FIGURE 1

```
                                                     MetLysHisLeuTrp
801                                                  ATGAAGCATCTGTG
                                                     TACTTCGTAGACAC

      ·PhePheLeuLeuLeuValAlaAlaProArgTrpValLeuSerGlnValGln
851   GTTCTTCCTTCTCCTAGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGC
      CAAGAAGGAAGAGGATCACCGTCGAGGGTCTACCCAGGACAGGGTCCACG

      ··LeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSer
901   AGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCC
      TCGACGTCCTCAGCCCGGGTCCTGACCACTTCGGAAGCCTCTGGGACAGG

      LeuThrCysThrValSerGlyAlaSerIleSerSerTyrTyrTrpSerTrp
951   CTCACCTGCACTGTCTCTGGTGCCTCCATCAGTAGTTACTACTGGAGCTG
      GAGTGGACGTGACAGAGACCACGGAGGTAGTCATCAATGATGACCTCGAC

      ·IleArgGlnProProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrTyr
1001  GATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATT
      CTAGGCCGTCGGGGGTCCCTTCCCTGACCTCACCTAACCCATATAGATAA

      ··SerGlySerThrAsnTyrAsnProSerLeuLysSerArgValThrIle
1051  ACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATA
      TGTCACCCTCGTGGTTGATGTTGGGGAGGGAGTTCTCAGCTCAGTGGTAT

      SerValAspThrSerLysAsnGlnPheSerLeuLysLeuArgSerValThr
1101  TCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGGTCTGTGAC
      AGTCATCTGTGCAGGTTCTTGGTCAAGAGGGACTTCGACTCCAGACACTG

      ·AlaAlaAspThrAlaValTyrTyrCysAlaArgGluArgLeuGlyIleGly
1151  CGCTGCGGACACGGCCGTGTATTACTGTGCGAGAGAGCGACTGGGGATCG
      GCGACGCCTGTGCCGGCACATAATGACACGCTCTCTCGCTGACCCCTAGC

      ··AspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThr
1201  GGGACTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCAGCCTCCACC
      CCCTGATGACCCCGGTTCCTTGGGACCAGTGGCAGAGGAGTCGGAGGTGG

      LysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu
1251  AAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCTAGAAGCACCTCCGA
      TTCCCGGGTAGCCAGAAGGGGGACCGCGGGACGAGATCTTCGTGGAGGCT

      ·SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProVal
1301  GAGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG
      CTCGTGTCGGCGGGACCCGACGGACCAGTTCCTGATGAAGGGGCTTGGCC

      ··ThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPhe
1351  TGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTC
      ACTGCCACAGCACCTTGAGTCCGCGAGACTGGTCGCCGCACGTGTGGAAG
```

FIGURE 1 Continuation

```
      ProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThr
1401  CCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAC
      GGTCGACAGGATGTCAGGAGTCCTGAGATGAGGGAGTCGTCGCACCACTG

      ·ValProSerSerAsnPheGlyThrGlnThrTyrThrCysAsnValAspHis
1451  CGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATC
      GCACGGGAGGTCGTTGAAGCCGTGGGTCTGGATGTGGACGTTGCATCTAG

      ··LysProSerAsnThrLysValAspLysThrVal
1501  ACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCT
      TGTTCGGGTCGTTGTGGTTCCACCTGTTCTGTCAACCACTCTCCGGTCGA

1551  CAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGA
      GTCCCTCCCTCCCACAGACGACCTTCGGTCCGAGTCGGGAGGACGGACCT

1601  CGCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATC
      GCGTGGGGCCGACACGTCGGGGTCGGGTCCCGTCGTTCCGTCCGGGGTAG

1651  TGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAG
      ACAGAGGAGTGGGCCTCCGGAGACGGGCGGGGTGAGTACGAGTCCCTCTC

1701  GGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCC
      CCAGAAGACCGAAAAAGGTGGTCCGAGGTCCGTCCGTGTCCGACCCACGG

1751  CCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGC
      GGATGGGGTCCGGGAAGTGTGTGTCCCCGTCCACGAACCGAGTCTGGACG

1801  CAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAA
      GTTTTCGGTATAGGCCCTCCTGGGACGGGGACTGGATTCGGCTGGGGTTT

1851  GGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATC
      CCGGTTTGACAGGTGAGGGAGTCGAGCCTGTGGAAGAGAGGAGGGTCTAG

                                      GluArgLysCysCysValGluCys
1901  CGAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTG
      GCTCATTGAGGGTTAGAAGAGAGACGTCTCGCGTTTACAACACAGCTCAC

      ·ProProCysPro
1951  CCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGC
      GGGTGGCACGGGTCCATTCGGTCGGGTCCGGAGCGGGAGGTCGAGTTCCG

2001  GGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTGGG
      CCCTGTCCACGGGATCTCATCGGACGTAGGTCCCTGTCCGGGGTCGACCC
```

FIGURE 1 Continuation

```
                                            AlaProProValAlaGlyPro
2051    TGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCACCTGTGGCAGGAC
        ACGACTGTGCAGGTGGAGGTAGAGAAGGAGTCGTGGTGGACACCGTCCTG

        ··SerValPheLeuPheProProLysProLysAspThrLeuMetIleSer
2101    CGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC
        GCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG

        ArgThrProGluValThrCysValValValAspValSerHisGluAspPro
2151    CGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCC
        GCCTGGGGACTCCAGTGCACGCACCACCACCTGCACTCGGTGCTTCTGGG

        ·GluValGlnPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLys
2201    CGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA
        GCTCCAGGTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT

        ··ThrLysProArgGluGluGlnPheAsnSerThrPheArgValValSer
2251    AGACAAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGC
        TCTGTTTCGGTGCCCTCCTCGTCAAGTTGTCGTGCAAGGCACACCAGTCG

        ValLeuThrValValHisGlnAspTrpLeuAsnGlyLysGluTyrLysCys
2301    GTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTG
        CAGGAGTGGCAACACGTGGTCCTGACCGACTTGCCGTTCCTCATGTTCAC

        ·LysValSerAsnLysGlyLeuProAlaProIleGluLysThrIleSerLys
2351    CAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCA
        GTTCCAGAGGTTGTTTCCGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT

        ··ThrLys
2401    AAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCG
        TTTGGTTTCCACCCTGGGCGCCCCATACTCCCGGTGTACCTGTCTCCGGC

2451    GCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCC
        CGAGCCGGGTGGGAGACGGGACCCTCACTGGCGACACGGTTGGAGACAGG

              GlyGlnProArgGluProGlnValTyrThrLeuProProSerArg
2501    CTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
        GATGTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCC

        GluGluMetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPhe
2551    GAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTT
        CTCCTCTACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA

        ·TyrProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGluAsn
2601    CTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA
        GATGGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCT

        ··AsnTyrLysThrThrProProMetLeuAspSerAspGlySerPhePhe
```

FIGURE 1 Continuation

```
2651  ACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTC
      TGTTGATGTTCTGGTGTGGAGGGTACGACCTGAGGCTGCCGAGGAAGAAG

      LeuTyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnVal
2701  CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGT
      GAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCA

      PheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLys
2751  CTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA
      GAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT

      SerLeuSerLeuSerProGlyLys
2801  AGAGCCTCTCCCTGTCTCCGGGTAAA
      TCTCGGAGAGGGACAGAGGCCCATTT
```

FIGURE 2

```
                MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrp
901             ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCT
                TACTCCCAGGGGCGAGTCGAGGACCCCGAGGACGACGAGA

        ··PheProGlyAlaArgCysLysLeuAspIleGlnLeuThrGlnSerPro
951     GGTTCCCAGGTGCCAGGTGTAAGCTTGACATCCAGCTGACCCAATCTCCA
        CCAAGGGTCCACGGTCCACATTCGAACTGTAGGTCGACTGGGTTAGAGGT

        SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla
1001    TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGC
        AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCCG

        ·SerGlnGlyIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
1051    AAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGA
        TTCAGTCCCGTAATCTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT

        ··AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
1101    AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
        TTCGGGGATTCGCGGACTAGATACGACGTAGGTCAAACGTTTCACCCCAG

        ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
1151    CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAAT
        GGTAGTTCCAAGTCGCCGTCACCTAGACCCTGTCTTAAGTGAGAGTGTTA

        ·SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
1201    CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
        GTCGTCGGACGTCGGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

        ··ThrTyrProProThrPheGlyGlnGlyThrLysValGluIleLysArg
1251    ATACTTACCCTCCGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGA
        TATGAATGGGAGGCTGCAAGCCGGTTCCCTGGTTCCACCTTTAGTTTGCT

        ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
1301    ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
        TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

        ·LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
1351    GAAATCTGGAACTGCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
        CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

        ··GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
1401    GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAAC
        CTCTCCGGTTTCATGTCACCTTCCACCTATTGCGGGAGGTTAGCCCATTG
```

FIGURE 2 Continuation

```
      SerGlnGluSer
1451  TCCCAGGAGAGT
      AGGGTCCTCTCA
```

FIGURE 3

```
                                            MetGluLeuGlyLeu
801                                         ATGGAATTGGGGCT
                                            TACCTTAACCCCGA

     ·ArgTrpValPheLeuValAlaLeuLeuArgGlyValGlnCysGlnValGln
851  CCGCTGGGTTTTCCTCGTTGCTCTTTTAAGAGGTGTCCAGTGTCAGGTGC
     GGCGACCCAAAAGGAGCAACGAGAAAATTCTCCACAGGTCACAGTCCACG

     ··LeuValGluSerGlyGlyGlyValValGlnProGlyArgSerLeuArg
901  AGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGA
     TCGACCACCTCAGACCCCCTCCGCACCAGGTCGGACCCTCCAGGGACTCT

     LeuSerCysValAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrp
951  CTCTCCTGTGTAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTG
     GAGAGGACACATCGGAGACCTAAGTGGAAGTCATCGATACCGTACGTGAC

     ·ValArgGlnAlaProGlyLysGlyLeuGluTrpValAlaValIleSerTyr
1001 GGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCAT
     CCAGGCGGTCCGAGGTCCGTTCCCCGACCTCACCCACCGTCAATATAGTA

     ··AspGlySerAsnLysTyrTyrAlaAspSerValLysGlyArgPheThr
1051 ATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACC
     TACTACCTTCATTATTTATGATACGTCTGAGGCACTTCCCGGCTAAGTGG

     IleSerArgAspAsnSerLysAsnThrLeuTyrLeuGlnMetAsnSerLeu
1101 ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCT
     TAGAGGTCTCTGTTAAGGTTCTTGTGCGACATAGACGTTTACTTGTCGGA

     ·ArgValGluAspThrAlaValTyrTyrCysAlaArgAspHisGlyGlyArg
1151 GAGAGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGA
     CTCTCAACTCCTGTGCCGACACATAATGACACGCTCTCTAGTGCCACCCT

     ··TyrValTyrAspTyrGlyMetAspValTrpGlyGlnGlyThrThrVal
1201 GGTACGTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTC
     CCATGCAGATGCTGATGCCATACCTGCAGACCCCGGTTCCCTGGTGCCAG

     ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaPro
1251 ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCC
     TGGCAGAGGAGTCGGAGGTGGTTCCCGGGTAGCCAGAAGGGGGACCGCGG

     ·CysSerArgSerThrSerGluSerThrAlaAlaLeuGlyCysLeuValLys
1301 CTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCTGGTCA
     GACGAGATCTTCGTGGAGGCTCTCGTGTCGGCGGGACCCGACGGACCAGT

     ··AspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeu
1351 AGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTG
     TCCTGATGAAGGGGCTTGGCCACTGCCACAGCACCTTGAGTCCGCGAGAC
```

FIGURE 3 Continuation

```
     ThrSerGlyValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyr
1401 ACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTA
     TGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGTCAGGAGTCCTGAGAT

     ·SerLeuSerSerValValThrValProSerSerAsnPheGlyThrGlnThr
1451 CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGA
     GAGGGAGTCGTCGCACCACTGGCACGGGAGGTCGTTGAAGCCGTGGGTCT

     ··TyrThrCysAsnValAspHisLysProSerAsnThrLysValAspLys
1501 CCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAG
     GGATGTGGACGTTGCATCTAGTGTTCGGGTCGTTGTGGTTCCACCTGTTC

     ThrVal
1551 ACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCA
     TGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCCACAGACGACCTTCGGT

1601 GGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCCCAG
     CCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACACGTCGGGGTCGGGTC

1651 GGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGC
     CCGTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGCCTCCGGAGACGGGCG

1701 CCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCA
     GGGTGAGTACGAGTCCCTCTCCCAGAAGACCGAAAAAGGTGGTCCGAGGT

1751 GGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGC
     CCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGGAAGTGTGTGTCCCCG

1801 AGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCC
     TCCACGAACCGAGTCTGGACGGTTTTCGGTATAGGCCCTCCTGGGACGGG

1851 CTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGA
     GACTGGATTCGGCTGGGGTTTCCGGTTTGACAGGTGAGGGAGTCGAGCCT

                                                   Glu
1901 CACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGCAGA
     GTGGAAGAGAGGAGGGTCTAGGCTCATTGAGGGTTAGAAGAGAGACGTCT

     ·ArgLysCysCysValGluCysProProCysPro
1951 GCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGCCAGCCCAGG
     CGCGTTTACAACACAGCTCACGGGTGGCACGGGTCCATTCGGTCGGGTCC

2001 CCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATC
     GGAGCGGGAGGTCGAGTTCCGCCCTGTCCACGGGATCTCATCGGACGTAG

2051 CAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCT
     GTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGTGGAGGTAGAGAAGGA
```

FIGURE 3 Continuation

```
      AlaProProValAlaGlyProSerValPheLeuPheProProLysPro
2101  CAGCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCC
      GTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGG

      LysAspThrLeuMetIleSerArgThrProGluValThrCysValValVal
2151  AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGT
      TTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGCACGCACCACCA

      ·AspValSerHisGluAspProGluValGlnPheAsnTrpTyrValAspGly
2201  GGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACG
      CCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGTTGACCATGCACCTGC

      ··ValGluValHisAsnAlaLysThrLysProArgGluGluGlnPheAsn
2251  GCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAAC
      CGCACCTCCACGTATTACGGTTCTGTTTCGGTGCCCTCCTCGTCAAGTTG

      SerThrPheArgValValSerValLeuThrValValHisGlnAspTrpLeu
2301  AGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCT
      TCGTGCAAGGCACACCAGTCGCAGGAGTGGCAACACGTGGTCCTGACCGA

      ·AsnGlyLysGluTyrLysCysLysValSerAsnLysGlyLeuProAlaPro
2351  GAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC
      CTTGCCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCCGGAGGGTCGGG

      ··IleGluLysThrIleSerLysThrLys
2401  CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGA
      GGTAGCTCTTTTGGTAGAGGTTTTGGTTTCCACCCTGGGCGCCCCATACT

2451  GGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGA
      CCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGAGACGGGACCCTCACT

                                  GlyGlnProArgGluProGlnVal
2501  CCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCACAGGTG
      GGCGACACGGTTGGAGACAGGGATGTCCCGTCGGGGCTCTTGGTGTCCAC

      TyrThrLeuProProSerArgGluGluMetThrLysAsnGlnValSerLeu
2551  TACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCT
      ATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTTCTTGGTCCAGTCGGA

      ·ThrCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGlu
2601  GACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGG
      CTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGCACCTCACCC

      ··SerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProMetLeu
2651  AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG
      TCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGTGGAGGGTACGAC

      AspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSer
2701  GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAG
```

FIGURE 3 Continuation

```
        CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTC

        ·ArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeu
2751    CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTC
        GTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAG

        ··HisAsnHisTyrThrGlnLysSerLeuSerLeuSerProGlyLys
2801    TGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
        ACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT
```

FIGURE 4

```
     MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPhePro
901  ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGTTCC
     TACTCCCAGGGGCGAGTCGAGGACCCCGAGGACGACGAGACCAAGG

     ··GlySerArgCysAspIleGlnMetThrGlnSerProSerSerValSer
951  CAGGTTCCAGATGCGACATCCAGATGACCCAATCTCCATCTTCCGTGTCT
     GTCCAAGGTCTACGCTGTAGGTCTACTGGGTTAGAGGTAGAAGGCACAGA

     AlaSerIleGlyAspArgValSerIleThrCysArgAlaSerGlnGlyIle
1001 GCATCTATAGGAGACAGAGTCTCCATCACTTGTCGGGCGAGTCAGGGTAT
     CGTAGATATCCTCTGTCTCAGAGGTAGTGAACAGCCCGCTCAGTCCCATA

     ·SerSerTrpLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProThrLeu
1051 TAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTACGC
     ATCGTCGACCAATCGGACCATAGTCGTCTTTGGTCCCTTTCGGGGATGCG

     ··LeuIleTyrAlaAlaSerThrLeuGlnArgGlyValProSerArgPhe
1101 TCCTTATCTATGCTGCATCCACTTTGCAACGTGGGGTCCCATCAAGGTTC
     AGGAATAGATACGACGTAGGTGAAACGTTGCACCCCAGGGTAGTTCCAAG

     SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGln
1151 AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCA
     TCGCCGTCACCTAGACCCTGTCTAAAGTGAGAGTGGTAGTCGTCGGACGT

     ·ProGluAspPheAlaThrTyrPheCysGlnGlnAlaAsnSerPheProPhe
1201 GCCTGAAGATTTTGCAACTTACTTTTGTCAACAGGCTAACAGTTTCCCAT
     CGGACTTCTAAAACGTTGAATGAAAACAGTTGTCCGATTGTCAAAGGGTA

     ··ThrPheGlyProGlyThrLysValAspIleLysArgThrValAlaAla
1251 TCACTTTCGGCCCTGGGACCAAAGTGGATATCAAACGAACTGTGGCTGCA
     AGTGAAAGCCGGGACCCTGGTTTCACCTATAGTTTGCTTGACACCGACGT

     ProSerValPheIlePheProProSerAspGluGlnLeuLysSerGlyThr
1301 CCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAC
     GGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTG

     ·AlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysVal
1351 TGCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAG
     ACGATCGCAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTC

     ··GlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSer
1401 TACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGT
     ATGTCACCTTCCACCTATTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCA

     ValThrGluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeu
1451 GTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCT
     CAGTGTCTCGTCCTGTCGTTCCTGTCGTGGATGTCGGAGTCGTCGTGGGA
```

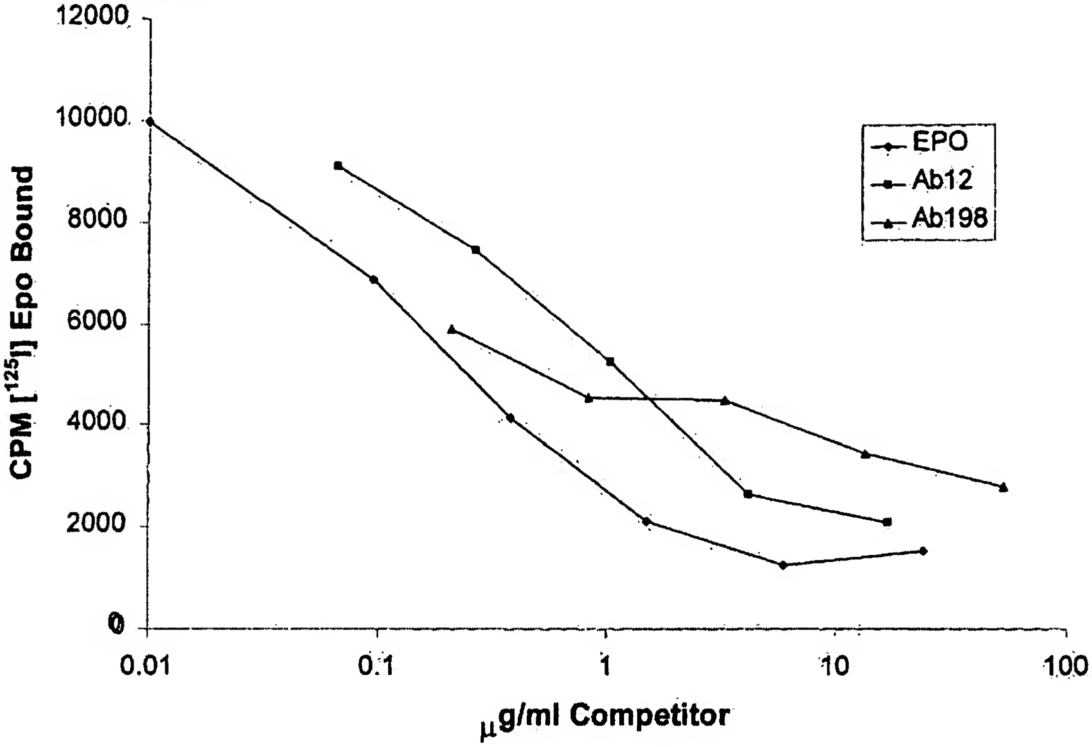
FIGURE 4 Continuation

```
     ·ThrLeuSerLysAlaAspTyrGluLysHisLysValTyrAlaCysGluVal
1501 GACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAG
     CTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGATGCGGACGCTTC

     ··ThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGly
1551 TCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGA
     AGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCGAAGTTGTCCCCT

     GluCys
1601 GAGTGT
     CTCACA
```

Figure 5



12000
10000
8000
6000
4000
2000
0
CPM [125I] Epo Bound
0.01
0.1
1
10
100
μg/ml Competitor
EPO
Ab12
Ab198

Erythropoietic Activity of Ab Candidates on F36e Human Erythroleukemic Cell Line

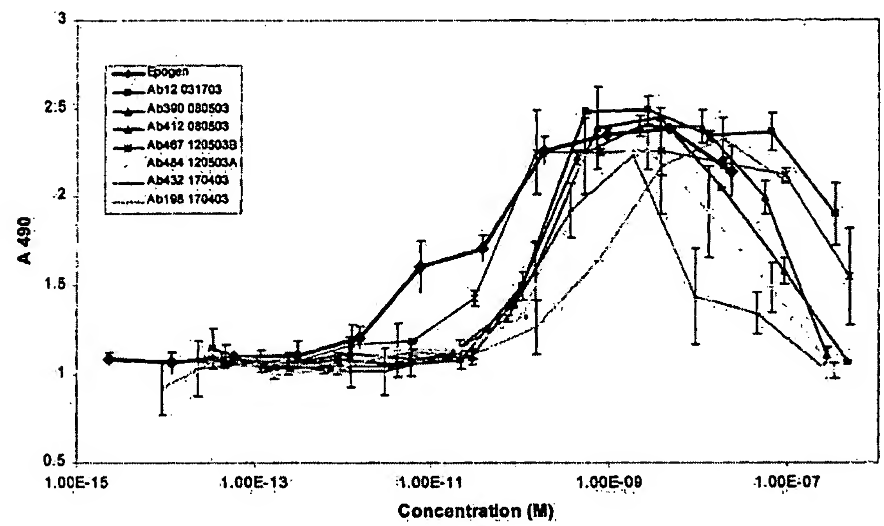
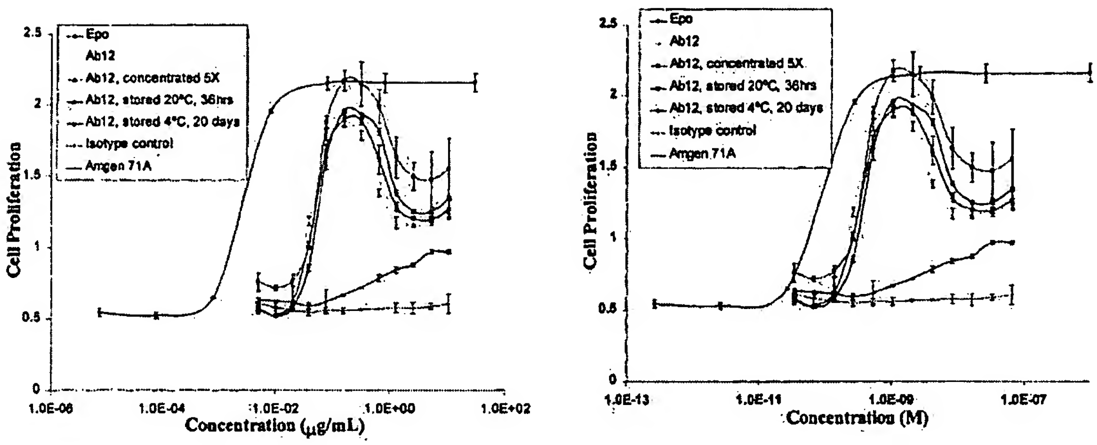


FIGURE 6

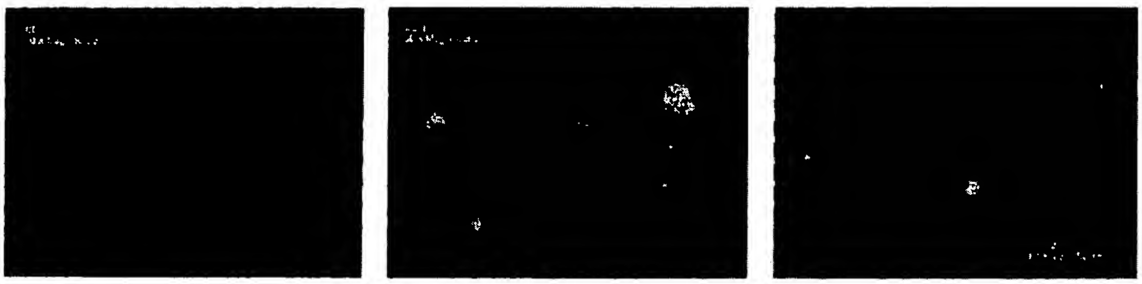
Figure 7



Epo
Ab12
Ab12, concentrated 5X
Ab12, stored 20°C, 36hrs
Ab12, stored 4°C, 20 days
Isotype control
Amgen 71A
Cell Proliferation
Concentration (μg/mL)
Concentration (M)

Figure 8

No Epo Control　　3 U/ml Epo　　500 ng/ml Ab12



150 colonies / dish　　48 colonies / dish

Figure 9

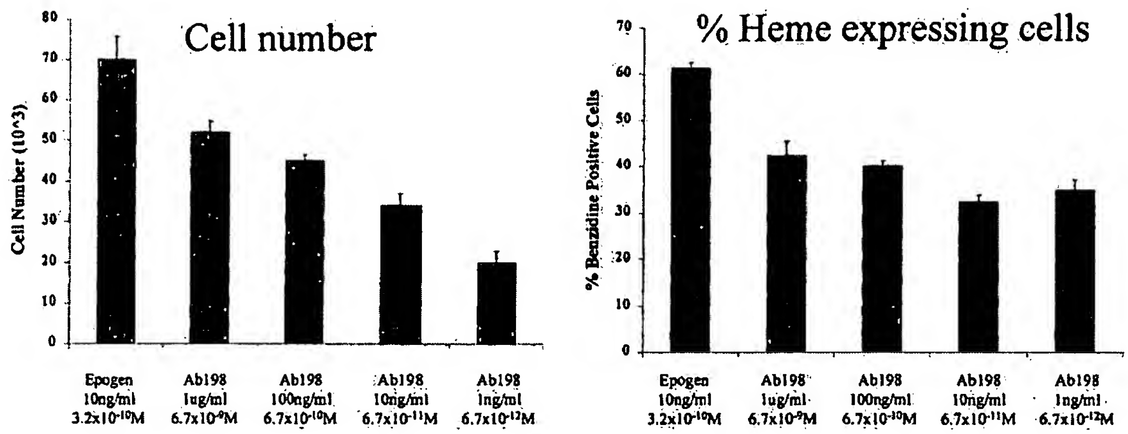

Cell number
Cell Number (10^3)
80
70
60
50
40
30
20
10
0
Epogen
10ng/ml
3.2x10-10M
Ab198
1ug/ml
6.7x10-9M
Ab198
100ng/ml
6.7x10-10M
Ab198
10ng/ml
6.7x10-11M
Ab198
1ng/ml
6.7x10-12M
% Heme expressing cells
% Benzidine Positive Cells
70
60
50
40
30
20
10
0
Epogen
10ng/ml
3.2x10-10M
Ab198
1ug/ml
6.7x10-9M
Ab198
100ng/ml
6.7x10-10M
Ab198
10ng/ml
6.7x10-11M
Ab198
1ng/ml
6.7x10-12M

Figure 10

No Epo Control | 3 U/ml Epo | 3200 ng/ml Ab12

Figure 11

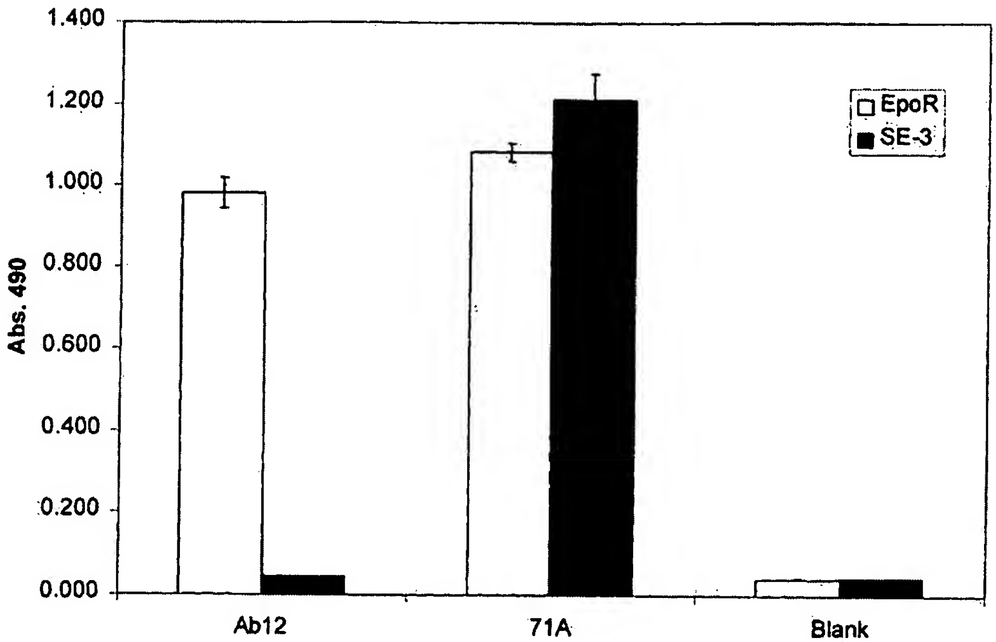

1.400
1.200
1.000
0.800
0.600
0.400
0.200
0.000
Abs. 490
EpoR
SE-3
Ab12
71A
Blank

Figure 12

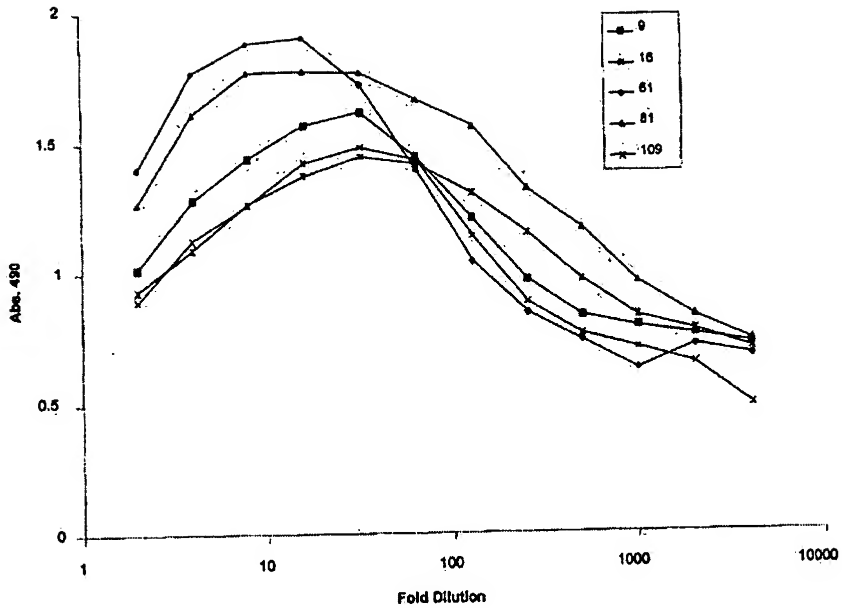

2
1.5
1
0.5
0
Abs. 490
1
10
100
1000
10000
Fold Dilution
9
16
61
81
109

Figure 13

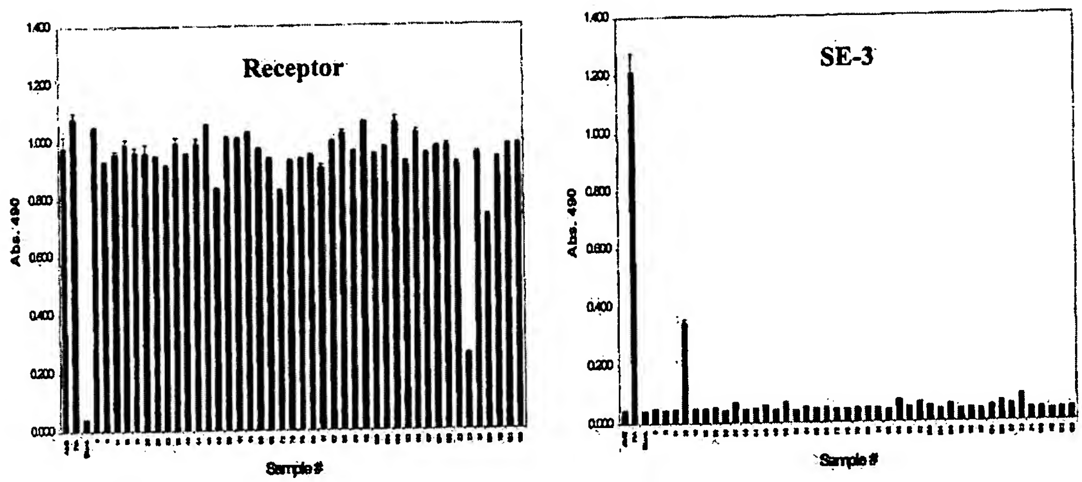

Receptor
SE-3
Abs. 490
Sample #
0.000
0.200
0.400
0.600
0.800
1.000
1.200
1.400

Figure 14

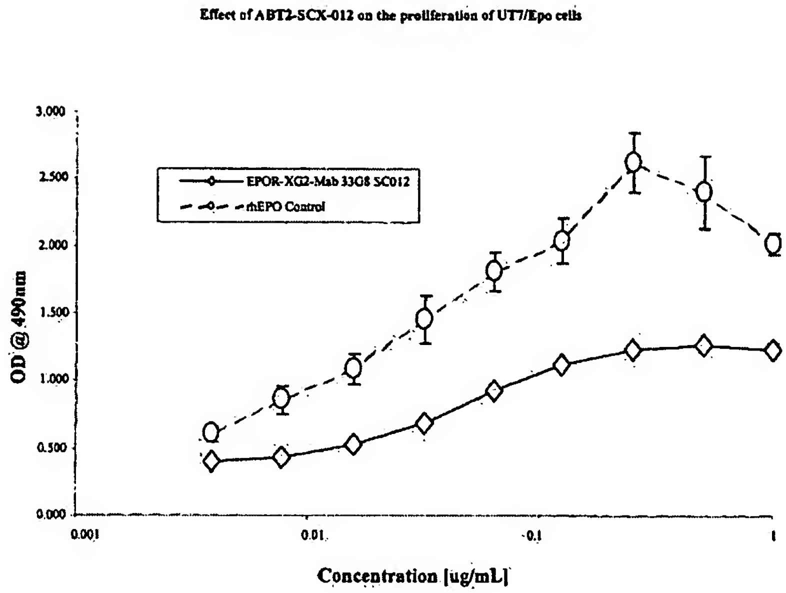

Effect of ABT2-SCX-012 on the proliferation of UT7/Epo cells
3.000
2.500
2.000
1.500
1.000
0.500
0.000
OD @ 490nm
EPOR-XG2-Mab 33G8 SC012
rhEPO Control
0.001
0.01
0.1
1
Concentration [ug/mL]

Figure 15

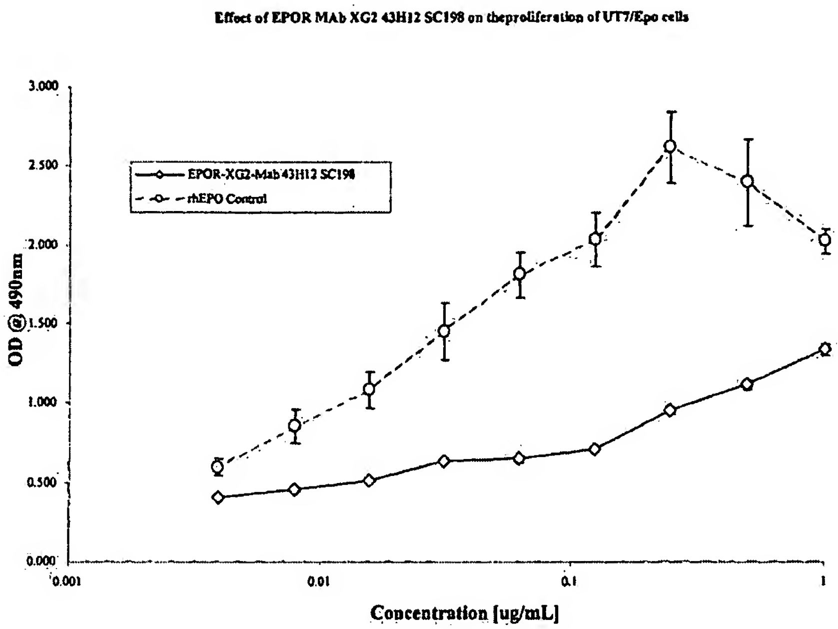
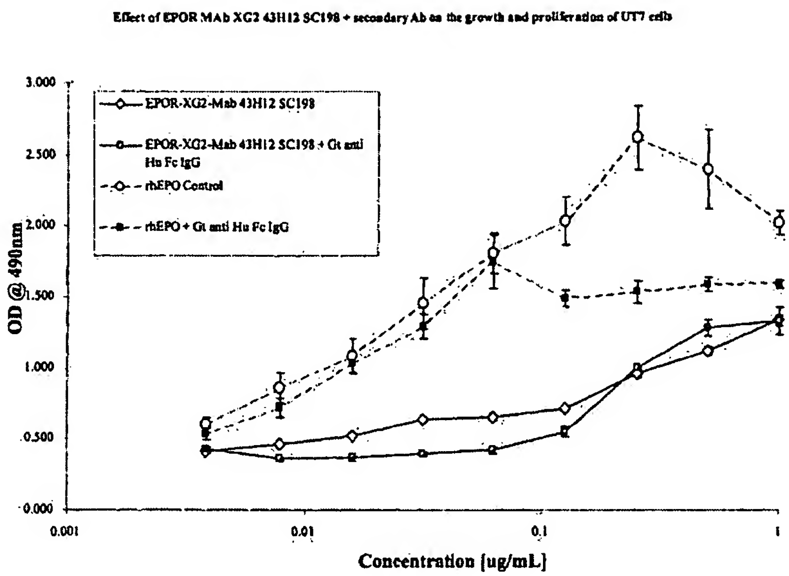
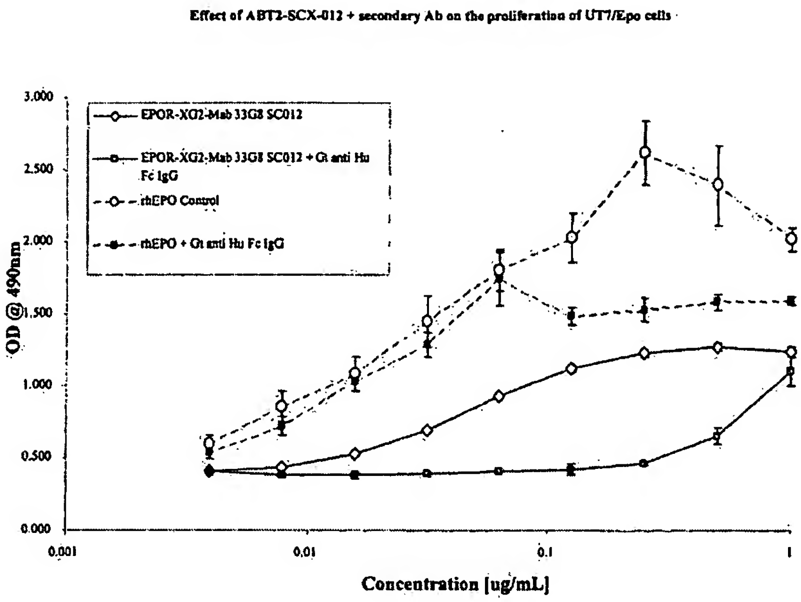

Effect of EPOR MAb XG2 43H12 SC198 on theproliferation of UT7/Epo cells
EPOR-XG2-Mab 43H12 SC198
rhEPO Control
3.000
2.500
2.000
1.500
1.000
0.500
0.000
OD @ 490nm
0.001
0.01
0.1
1
Concentration [ug/mL]

Figure 16



Effect of EPOR MAb XG2 43H12 SC198 + secondary Ab on the growth and proliferation of UT7 cells
EPOR-XG2-Mab 43H12 SC198
EPOR-XG2-Mab 43H12 SC198 + Gt anti Hu Fc IgG
rhEPO Control
rhEPO + Gt anti Hu Fc IgG
OD @ 490nm
3.000
2.500
2.000
1.500
1.000
0.500
0.000
0.001
0.01
0.1
1
Concentration [ug/mL]

Figure 17



Effect of ABT2-SCX-012 + secondary Ab on the proliferation of UT7/Epo cells
EPOR-XG2-Mab 33G8 SC012
EPOR-XG2-Mab 33G8 SC012 + Gt anti Hu Fc IgG
rhEPO Control
rhEPO + Gt anti Hu Fc IgG
3.000
2.500
2.000
1.500
1.000
0.500
0.000
OD @ 490nm
0.001
0.01
0.1
1
Concentration [ug/mL]

FIGURE 18

A-- ABT2-SCX-003 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG 3'

B-- ABT2-SCX-003 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-003 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGTCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTGCGCTCCTAATCTATGCTGCATCCA
GTTTGCAGCGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGA
CTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTTT
GTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCAAAGTGGAT
ATCAAAC3'

D-- ABT2-SCX-003 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGDRVSITCRASQGISSWLVWYQQKPGKAPALLIYAASSLQ
RGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQANSFPFTFGPGTKVDIK

FIGURE 19

A-- ABT2-SCX-012 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACC
CTGTCCCTCACCTGCACTGTCTCTGGTGCCTCCATCAGTAGTTACTACTGGAG
CTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTAT
TACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATAT
CAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGGTCTGTGACCGC
TGCGGACACGGCCGTGTATTACTGTGCGAGAGAGCGACTGGGGATCGGGGAC
TACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCAG3'

B-- ABT2-SCX-012 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSETLSLTCTVSGASISSYYWSWIRQPPGKGLEWIGYIYYSGS
TNYNPSLKSRVTISVDTSKNQFSLKLRSVTAADTAVYYCARERLGIGDYWGQGT
LVTVSS

C-- ABT2-SCX-012 Nucleotide sequence of light chain variable region:

5'GACATCCAGCTGACCCAATCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAG
AATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTAC
TGTCTACAGCATAATACTTACCCTCCGACGTTCGGCCAAGGGACCAAGGTGG
AAATCAAAC3'

D-- ABT2-SCX-012 Amino acid sequence of light chain variable region:

DIQLTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQS
GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNTYPPTFGQGTKVEIK

FIGURE 20

A-- ABT2-SCX-022 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGTAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-022 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVVVISY
DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-022 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTACGCTCCTAATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCAAAGTGGA
TATCAAAC3'

D-- ABT2-SCX-022 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGDRVSITCRASQGISSWLAWYQQKPGKAPTLLIYAASSLQ
RGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQANSFPFTFGPGTKVDIK

FIGURE 21

A-- ABT2-SCX-054 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTC
CCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAAATATGGCATGC
ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTTTATG
GTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACC
ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGTCCGTACTACTTTGA
CTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG3'

B-- ABT2-SCX-054 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSKYGMHWVRQAPGKGLEWVAVLW
YDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGPYYFDY
WGQGTLVTVSS

C-- ABT2-SCX-054 Nucleotide sequence of light chain variable region:

5'GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAA
GAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGC
CTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCA
TCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGA
CAGACTTCACTGTCACCATCAGCAGACTGGAACCTGAAGATTTTGCAGTGTAT
TACTGTCAGCAGTATGGTAGTTCACCGTGGACGTTCGGCCAAGGGACCAAGG
TGGAAATCAAAC3'

D-- ABT2-SCX-054 Amino acid sequence of light chain variable region:

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRA
TGIPDRFSGSGSGTDFTVTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

FIGURE 22

A-- ABT2-SCX-060 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-060 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-060 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCCGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTACGCTCCTAATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCAAAGTGGA
TATCAAAC3'

D-- ABT2-SCX-060 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGDRVSITCRASQGISSWLAWYQQKPGKAPTLLIYAASSLQ
RGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQANSFPFTFGPGTKVDIK

FIGURE 23

A-- ABT2-SCX-102 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-102 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-102 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCAAAGTGGA
TATCAAAC3'

D-- ABT2-SCX-102 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGDRVSITCRASQGISSWLAWYQQKPGKAPKRLIYAASSLQ
RGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQANSFPFTFGPGTKVDIK

FIGURE 24

A-- ABT2-SCX-135 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG 3'

B-- ABT2-SCX-135 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-135 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTACATCTGTAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTGGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGCAAGCCCCTACGCTCCTAATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGATTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAACAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCAAAGTGGA
TGTCAAAC3'

D-- ABT2-SCX-135 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSTSVGDRVSITCRASQGIGSWLAWYQQKPGQAPTLLIYAASSLQ

RGVPSRFSGSGSGTDFTLTINSLQPEDFATYFCQQANSFPFTFGPGTKVDVK

FIGURE 25

A-- ABT2-SCX-145 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-145 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-145 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTGGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGCAAGCCCCTACGCTCCTAATCTATGCTGCATCC
AGTTTGCAACGTGGGGTCCCATCAAGATTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAACAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCAAAGTGGA
TGTCAAAC3'

D-- ABT2-SCX-145 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGDRVSITCRASQGIGSWLAWYQQKPGQAPTLLIYAASSLQ

RGVPSRFSGSGSGTDFTLTINSLQPEDFATYFCQQANSFPFTFGPGTKVDVK

FIGURE 26

A-- ABT2-SCX-198 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGTAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-198 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCVASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDHGGRYVY
DYGMDVWGQGTTVTVSS

C-- ABT2-SCX-198 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAATCTCCATCTTCCGTGTCTGCATCTATAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTACGCTCCTTATCTATGCTGCATCC
ACTTTGCAACGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCAAAGTGGA
TATCAAAC3'

D-- ABT2-SCX-198 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASIGDRVSITCRASQGISSWLAWYQQKPGKAPTLLIYAASTLQR
GVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQANSFPFTFGPGTKVDIK

FIGURE 27

A-- ABT2-SCX-254 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGG
TTTGATGGAAATAATAAATTCTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTCGAGGACACGGCTGTGTATTACTGTGCGCGAGGCGGGAGCTACTGGGAC
TACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG3'

B-- ABT2-SCX-254 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWF
DGNNKFYADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCARGGSYWDY
WGQGTLVTVSS

C-- ABT2-SCX-254 Nucleotide sequence of light chain variable region:

5'GATATTGTGATGACCCAGACTCCACTCTTCTCATTTGTCATGATTGGACAGC
CGGCCTCCATCTCCTGCAGGTCTAGGCAAAGCCTCGTACACAGTGATGGAAA
CACCTACTTGAATTGGCTTCAGCAGAGGCCAGGCCAGCCTCCAAGACTCCTA
ATTTATAAGACTTCTAACCGGTTCTCTGGGGTCCCAGATAGATTCAGTGGCAG
TGGGGCAGGGACAGATTTCACACTGAAAATCAGCAGGGTGGAAGCTGAGGA
TGTCGGGGTTTATTACTGTATGCAAGCTACACAATTTCCTATCACGTTCGGCC
AAGGGACACGACTGGAGATTAAA3'

D-- ABT2-SCX-254 Amino acid sequence of light chain variable region:

DIVMTQTPLFSFVMIGQPASISCRSRQSLVHSDGNTYLNWLQQRPGQPPRLLIYKT
SNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQFPITFGQGTRLEI
K

FIGURE 28

A-- ABT2-SCX-267 Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCA
TATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAG
AGTTGAGGACACGGCTGTGTATTACTGTGCGAAAGATCACGGTGGGAGGTAC
GTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT
CCTCAG3'

B-- ABT2-SCX-267 Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRVEDTAVYYCAKDHGGRYV
YDYGMDVWGQGTTVTVSS

C-- ABT2-SCX-267 Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACA
GAGTCTCCATCACTTGTCGGGCGAGTCAGGGTATTGGCAGCTGGTTAGCCTG
GTATCAGCAGAAACCAGGGCAAGCCCCTACGCTCCTAATCTATGCTGCCTCC
AGTTTGCAACGTGGGGTCCCATCAAGATTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAACAGCCTGCAGCCTGAAGATTTTGCAACTTACTTT
TGTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCTGGGACCAAAGTGGA
TGTCAAAC3'

D-- ABT2-SCX-267 Amino acid sequence of light chain variable region:

DIQMTQSPSSVSASVGDRVSITCRASQGIGSWLAWYQQKPGQAPTLLIYAASSLQ
RGVPSRFSGSGSGTDFTLTINSLQPEDFATYFCQQANSFPFTFGPGTKVDVK

FIGURE 29

Single Cell	V Heavy/D/J	FR1	CDR1	FR2	CDR2
-	Germline	QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA	VISYDGSNKYYADSVKG
3	VH3-30(V3-30)/D4-23/LH6b	-------------------------	----------	--------------	-----------------
22		-------------------------	----------	-------------V	-----------------
60		-------------------------	----------	--------------	-----------------
102		-------------------------	----------	--------------	-----------------
135		-------------------------	----------	--------------	-----------------
145		-------------------------	----------	--------------	-----------------
198		----------------------V--	----------	--------------	-----------------
-	Germline	QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA	VISYDGSNKYYADSVKG
267	VH3-30.5(DP-49)/D4-23/JH6b	-------------------------	----------	--------------	-----------------
-	Germline	QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA	VISYDGSNKYYADSVKG
54	VH3-33(DP-50)/DIR3/JH4b	-------------------------	-----K----	--------------	-L---------------
254	VH3-33(DP-50)/D21-10rc/JH4b	-------------------------	----------	--------------	---F--N--F-------
-	Germline	QVQLQESGPGLVKPSETLSLTCTVS	GGSISSYYWS	WIRQPPGKGLEWIG	YIYYSGSTNYNPSLKS
12	VH4-59(DP-71)/DIR4rc/JM4a	-------------------------	-A--------	--------------	----------------

Single Cell	V Heavy/D/J	FR3	CDR3	FR4
-	Germline	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	DHGGRYVYDYGMDV	WGQGTTVTVSS
3	VH3-30(V3-30)/D4-23/LH6b	---------------------V----------	--------------	-----------
22		---------------------V----------	--------------	-----------
60		---------------------V----------	--------------	-----------
102		---------------------V----------	--------------	-----------
135		---------------------V----------	--------------	-----------
145		---------------------V----------	--------------	-----------
198		---------------------V----------	--------------	-----------
-	Germline	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK		WGQGTTVTVSS
267	VH3-30.5(DP-49)/D4-23/JH6b	---------------------V----------	--------------	-----------
-	Germline	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR		WGQGTLVTVSS
54	VH3-33(DP-50)/DIR3/JH4b	--------------------------------	GPYYFDY	-----------
254	VH3-33(DP-50)/D21-10rc/JH4b	---------------------V----------	GGSYWDY	-----------
-	Germline	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR		WGQGTLVTVSS
12	VH4-59(DP-71)/DIR4rc/JM4a	-----------------R--------------	ERLGIGDY	-----------

Figure 30

Single Cell	V Kappa/J	FR1	CDR1	FR2	CDR2
-	(Germline)	EIVLTQSPGTLSLSPGERATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY	GASSRAT
54	VkIII (A27)/Jk1	-----------------------	------------	---------------	-------
-	(Germline)	DIQMTQSPSSVSASVGDRVTITC	RASQGISSWLA	WYQQKPGKAPKLLIY	AASSLQS
3	VkI (L5)/Jk3	-------------------S---	----------V	----------A----	------R
22		-------------------S---	-----------	----------T----	------R
60		-------------------S---	-----------	----------T----	------R
102		-------------------S---	-----------	-----------R---	------R
135		------------T------S---	------G----	-------Q--T----	------R
145		-------------------S---	------G----	-------Q--T----	------R
198		--------------I----S---	-----------	----------T----	---T--R
267		-------------------S---	------Q----	-------Q--T----	------R
-	(Germline)	DIQMTQSPSSLSASVGDRVTITC	RASQGIRNDLG	WYQQKPGKAPKRLIY	AASSLQS
12	VkI (A30)/Jk1	---L-------------------	-----------	---------------	-------
-	(Germline)	DIVMTQTPLSSPVTLGQPASISC	RSSQSLVHSDGNTYLS	WLQQRPGQPPRLLIY	KISNRFS
254	VkII (A23)/Jk5	---------F-F-MI--------	--R------------N	---------------	-T-----

Single Cell	V Kappa/J	FR3	CDR3	J
-	(Germline)	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSPWT	FGQGTKVEIK
54	VkIII (A27)/Jk1	----------------V---------------	---------	----------
-	(Germline)	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQANSFPFT	FGPGTKVDIK
3	VkI (L5)/Jk3	------------------------------F-	---------	----------
22		------------------------------F-	---------	----------
60		------------------------------F-	---------	----------
102		------------------------------F-	---------	----------
135		-------------------N----------F-	---------	--------V-
145		-------------------N----------F-	---------	--------V-
198		------------------------------F-	---------	----------
267		-------------------N----------F-	---------	--------V-
-	(Germline)	GVPSRFSGSGSGTEFTLTISSLQPEDFATYYC	LQHNSYPPT	FGQGTKVEIK
12	VkI (A30)/Jk1	--------------------------------	----T----	----------
-	(Germline)	GVPDRFSGSGAGTDFTLKISRVEAEDVGVYYC	MQATQFPIT	FGQGTRLEIK
254	VkII (A23)/Jk5	--------------------------------	---------	----------

Comparison of Erythropoietic Activity of Gamma 1 Ab-12 versus Gamma 2 Ab-12 on F36e Human Erythroleukemic Cell Line

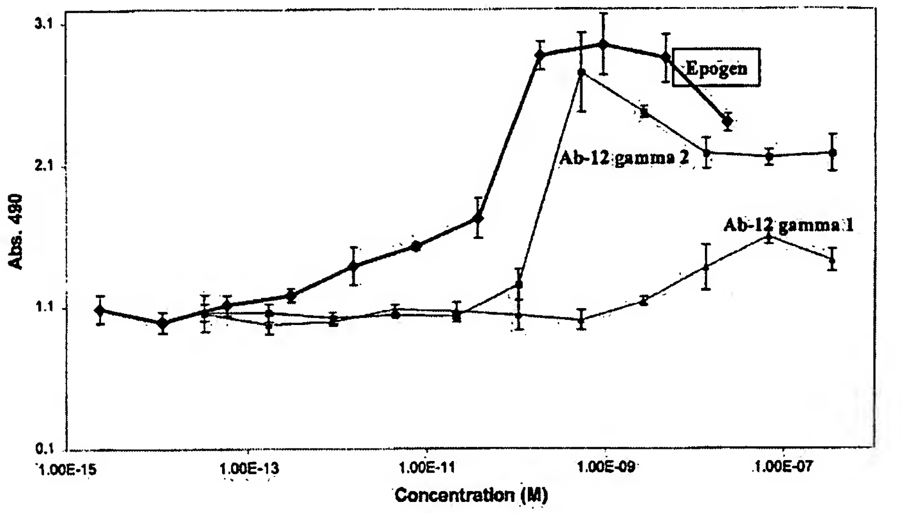
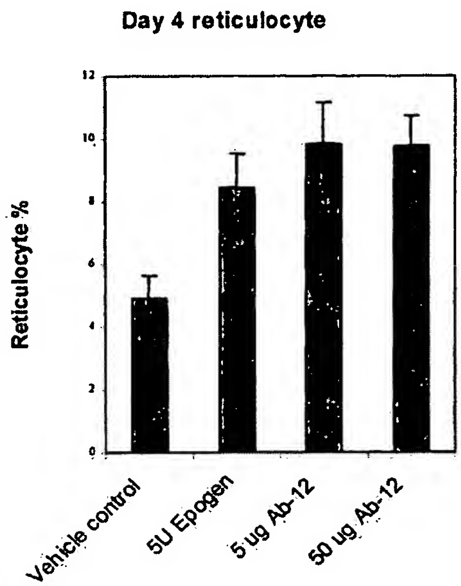


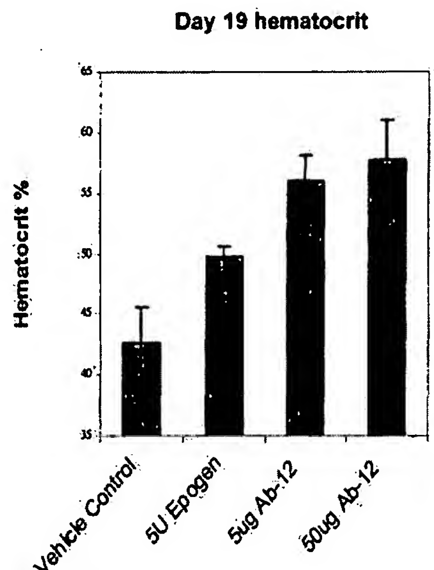
FIGURE 31

FIGURE 32

Ab-12 Increases Reticulocyte Count and Hematocrit in Transgenic Mice

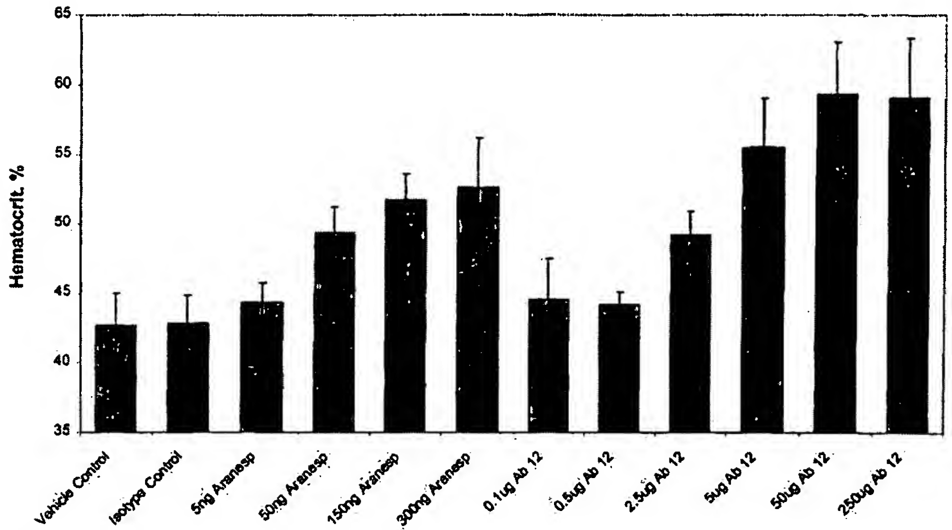


* P<0.001



* P< 0.001

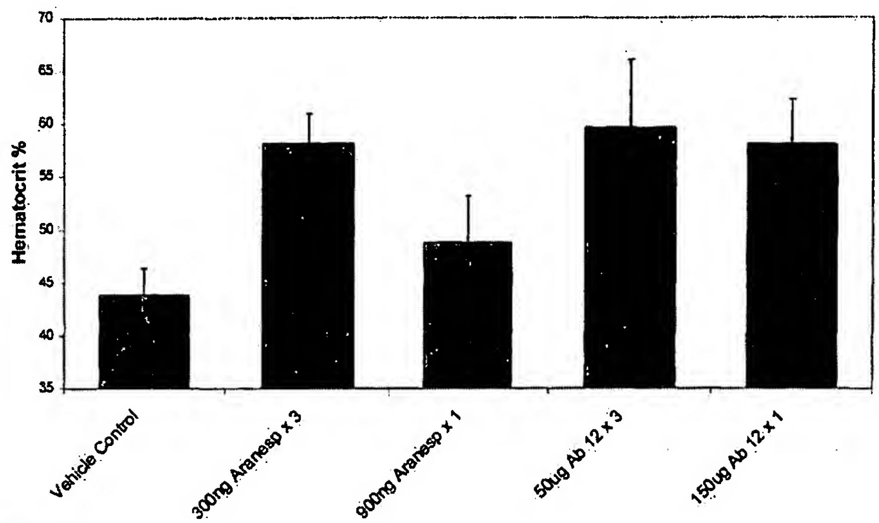
Day 19 Hematocrit in Transgenic Mice Following Weekly Dosing with Ab-12 or Aranesp



* P< 0.001

FIGURE 33

Day 19 Hematocrit in Transgenic Mice Comparing Single vs. Weekly Dosing with Ab-12 or Aranesp



* P< 0.01

FIGURE 34

FIGURE 35

A. Ab390 nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACC
CTGTCCCTCACCTGCACTGTCTCTGGTGCCTCCATCAGTAATTACTACTGG
AGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATGTC
TCTTACAGTGGGAGTACGTACTACAACCCCTCCCTCAAGGGTCGAGTCACC
ATGTCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTG
ACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGAGAAAAACTGGGGATT
GGAGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA3'

B. Ab390 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSETLSLTCTVSGASISNYYWSWIRQPPGKGLEWIGYVSYSGS
TYYNPSLKGRVTMSVDTSKNQFSLKLSSVTAADTAVYYCAREKLGIGDYWGQGTLV
TVSS

C. Ab390 nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAAAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAG
AATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTA
CTGTCTACAGCATAATAGTTATCCGTGCAGTTTTGGCCAGGGGACCAAGCTG
GAGATCAAAC3'

D. Ab390 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGWYQQKPGKAPKRLIYAASSLQS
GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPCSFGQGTKLEIK

FIGURE 36

A. Ab412 nucleotide sequence of heavy chain variable region:

5′ CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCC
TGTCCCTCACCTGCACTGTCTCTGGTGCCTCCATCAGCAGTGGTGCTTACTA
CTGGAGTTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTGGATTGGGTAC
ATCTATAAGAGTGAGACCTCCTACTACAACCCGTCCCTCAAGAGTCGACTTA
CCCTATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAACCTGATCTCTGT
GACTGCCGCGGACACGGCCGTGTATTATTGTGCGAGAGATAAACTGGGGATC
GCGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA3′

B. Ab412 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSQTLSLTCTVSGASISSGAYYWSWIRQHPGKGLEWIGY
IYKSETSYYNPSLKSRLTLSVDTSKNQFSLNLISVTAADTAVYYCARDKLGI
ADYWGQGTLVTVSS

C. Ab412 nucleotide sequence of light chain variable region:

5′ GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGACATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AATTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAG
AATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTA
CTGTCTACAGCATAATAGCTACCCTCCCACTTTCGGCGGAGGGACCAAGGTG
GAAATCAAAC3′

D. Ab412 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRASQDIRNDLGWYQQKPGKAPKRLIYAAS
NLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPPTFGGGTKV
EIK

FIGURE 37

A. Ab432 nucleotide sequence of heavy chain variable region:

5′CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCC
TGTCCCTCACCTGCACTGTCTCTGGTGTCTCCATCAGTAATTACTACTGGAG
CTGGATCCGGCAGTCCCCAGGGAAGGGACTGGAGTGGATTGGATATATCTAT
TACAGTGGGAGTCCCTATTACAACCCCTCCCTCAAGAGTCGAGTCACTATAT
CTGCAGACACGTCCAAGAACCAATTCTCCCTGAAGCTGAGCTCTGTGACCGC
TGCGGACACGGCCATTTATTACTGTGCGAGAGAAAAACTGGGGATTGGAGAC
TACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG3′

B. Ab432 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSETLSLTCTVSGVSISNYYWSWIRQSPGKGLEWIGYIY
YSGSPYYNPSLKSRVTISADTSKNQFSLKLSSVTAADTAIYYCAREKLGIGD
YWGQGTLVTVSS

C. Ab430 nucleotide sequence of light chain variable region:

5′GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTCGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAG
AATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTA
CTGTCTACAGCATAATAGTTACCCTCCCACTTTCGGCCCTGGGACCAAGGTG
GATATCAAAC3′

D. Ab430 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS
SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPPTFGPGTKV
DIK

FIGURE 38

A. Ab467 nucleotide sequence of heavy chain variable region:

5′ CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCC
TGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTCGTTACTACTGGAG
CTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATGTCTCT
TACAGTGGGAGCACCTACTACAACCCCTCCCTCAAGAGTCGAGTCACCATAT
CAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGC
TGCGGACACGGCCGTGTATTACTGTGCGAGAGATAAACTGGGGATTGGAGAC
TACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG3′

B. Ab467 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPSETLSLTCTVSGGSISRYYWSWIRQPPGKGLEWIGYVS
YSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDKLGIGD
YWGQGTLVTVSS

C. Ab467 nucleotide sequence of light chain variable region:

5′ GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCGGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAG
AATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTA
CTGTCTACAGCATAATAGTTACCCGTGCAGTTTTGGCCAGGGGACCAAGCTG
GAGATCAAAC3′

D. Ab467 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAAS
SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPCSFGQGTKL
EIK

FIGURE 39

A. Ab484 nucleotide sequence of heavy chain variable region:

5′CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTTACAGACCC
TGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTGGTGTTTACTA
CTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTGGATTGGGTAC
ATCTATAACAGTAAGACCTCCTATTATAATCCGTCCCTCAAGAGTCGACTTA
CCCTATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAACCTGATCTCTGT
GACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGATAAATTGGGGATC
GCGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG3′

B. Ab484 Amino acid sequence of heavy chain variable region:

QVQLQESGPGLVKPLQTLSLTCTVSGGSISSGVYYWSWIRQHPGKGLEWIGY
IYNSKTSYYNPSLKSRLTLSVDTSKNQFSLNLISVTAADTAVYYCARDKLGI
ADYWGQGTLVTVSS

C. Ab484 nucleotide sequence of light chain variable region:

5′GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACA
GAGTCACCATCACTTGCCGGACAAGTCAGGGCATTAGAAATGATTTAGGCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCC
AGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAG
AATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTA
CTGTCTACAGCATAATAGCTACCCTCCCACTTTCGGCGGAGGGACCAAGGTG
GAGATCAAAC3′

D. Ab484 Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRTSQGIRNDLGWYQQKPGKAPKRLIYAAS
SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPPTFGGGTKV
EIK

[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
-	-	[redacted]	-	QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA
43H12	198	14325.3	VH3-30/D4-23/JH6	----------------------V--	----------	--------------
-	-	[redacted]		QVQLQESGPGLVKPSETLSLTCTVS	GGSISSYYWS	WIRQPPGKGLEWIG
33G8	12	13308.1	VH4-59/DIR4RC/JH4	-------------------------	-A--------	--------------
-	-	[redacted]	-	QVQLQESGPTLVKPSQTLSLTCTVS	GGSISSGGYYWS	WIRQHPGKGLEWIG
230A4	412	54995.1	V4-31/DIR4rc/JH4	---------G---------------	-A-----A----	--------------
-	-	[redacted]	-	QVQLQESGPGLVKPSQTLSLTCTVS	GGSISSGGYYWS	WIRQHPGKGLEWIG
208A12	484	57130.1	V4-30.1/DIR4rc/JH4	---------------L---------	-------V----	--------------
-	-	[redacted]	-	QVQLQESGPGLVKPSETLSLTCTVS	GGSISSYYWS	WIRQPPGKGLEWIG
259C12	467	56977.2	V4-59/D7-27/JH4	-------------------------	-----R----	--------------
236D12	390	57141.2	VH4-59/D7-27/JH4b	-------------------------	-A---N----	--------------
223H2	432	57354.11	VH4-59/D7-27/JH4b	-------------------------	-V---N----	----S---------

	[illegible]	[illegible]	[illegible]	[illegible]
	VISYDGSNKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK		WGQGTTVTVSS
198	-----------------	----------------------V--------R	DWGGRYVYDYGMDV	-----------
	YIYYSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR		WGQGTLVTVSS
16	----------------	----------------R---------------	ERLGIGDY	-----------
	YIYYSGSTYYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR		WGQGTLVTVSS
412	---K-ETS--------	-L-L-----------N-I--------------	DKLGIADY	-----------
	YIYYSGSTYYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR		WGQGTLVTVSS
484	---N-KTS--------	-L-L-----------N-I--------------	DKLGIADY	-----------
	YIYYSGSTNYNPSLKG	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR		WGQGTLVTVSS
467	-VS-----Y-------	--------------------------------	DKLGIGDY	-----------
390	-VS-----Y------G	---M----------------------------	EKLGIGDY	-----------
430	-------PY-------	-----A-----------------------I--	EKLGIGDY	-----------

Figure 40

[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
-	-	[redacted]	-	DIQMTQSPSSVSASVGDRVTITC	RASQGISSWLA	WYQQKPGKAPKLLIY
43H12	198	54325.3	L5/Jk3	--------------I----S---	-----------	----------T----
-	-	[redacted]	-	DIQMTQSPSSLSASVGDRVTITC	RASQGIRNDLG	WYQQKPGKAPKRLIY
33D8	12	53308.1	A30/Jk3	---L-------------------	-----------	---------------
233H2	430	54494.1	A30/Jk3	-----------------------	-----------	---------------
-	-	[redacted]	-	DIQMTQSPSSLSASVGDRVTITC	RASQGIRNDLG	WYQQKPGKAPKRLIY
23CA4	412	54732.2	A30(Vk1)/Jk4	-----------------------	----D------	---------------
-	-	[redacted]	-	DIQMTQSPSSLSASVGDRVTITC	RASQGIRNDLG	WYQQKPGKAPKRLIY
208A12	484	57094.1	A30(Vk1)/Jk4	-----------------------	-T---------	---------------
-	-	[redacted]	-	DIQMTQSPSSLSASVGDRVTITC	RASQGIRNDLG	WYQQKPGKAPKRLIY
259C12	467	56956.1	A30(Vk1)/Jk2	-----------------------	-----------	---------------
236D12	390	56829.3	A30(Vk1)/Jk2	-----------------------	------K----	---------------

	[illegible]	[illegible]	[illegible]	[illegible]
	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQANSFPPT	FGPGTKVDIK
198	---T--R	------------------------------P-	---------	----------
	AASSLQS	GVPSRFSGSGSGTEFTLTISSLQPEDFATYYC	LQHNSYPPT	FGQGTKVEIK
12	-------	--------------------------------	----T--P-	----------
430	-------	--------------------------------	-------P-	--P----D--
	AASSLQS	GVPSRFSGSGSGTEFTLTISSLQPEDFATYYC	LQHNSYPLT	FGGGTKVEIK
412	---N---	--------------------------------	-------P-	----------
	AASSLQS	GVPSRFSGSGSGTEFTLTISSLQPEDFATYYC	LQHNSYPLT	FGQGTKVEIK
484	-------	--------------------------------	-------P-	----------
	AASSLQS	GVPSRFSGSGSGTEFTLTISSLQPEDFATYYC	LQHNSYPLT	FGQGTRLEIK
464	-------	--------------------------------	-------CS	----------
390	-------	--------------------------------	-------CS	----------

Figure 41

FIGURE 42

```
                 MetLysHisLeuTrpPhePheLeuLeuLeuValAla
1                ATGAAGCATCTGTGGTTCTTCCTTCTCCTGGTGG
                 TACTTCGTAGACACCAAGAAGGAAGAGGACCACC

     ··AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
51   CAGCTCCCAGATGGGTCCTGTCCCAGGTGCAGCTGCAGGAGTCGGGCCCA
     GTCGAGGGTCTACCCAGGACAGGGTCCACGTCGACGTCCTCAGCCCGGGT

     GlyLeuValLysProSerGluThrLeuSerLeuThrCysThrValSerGly
101  GGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGG
     CCTGACCACTTCGGAAGCCTCTGGGACAGGGAGTGGACGTGACAGAGACC

     ·AlaSerIleSerAsnTyrTyrTrpSerTrpIleArgGlnProProGlyLys
151  TGCCTCCATCAGTAATTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGA
     ACGGAGGTAGTCATTAATGATGACCTCGACCTAGGCCGTCGGGGGTCCCT

     ··GlyLeuGluTrpIleGlyTyrValSerTyrSerGlySerThrTyrTyr
201  AGGGACTGGAGTGGATTGGGTATGTCTCTTACAGTGGGAGTACGTACTAC
     TCCCTGACCTCACCTAACCCATACAGAGAATGTCACCCTCATGCATGATG

     AsnProSerLeuLysGlyArgValThrMetSerValAspThrSerLysAsn
251  AACCCCTCCCTCAAGGGTCGAGTCACCATGTCAGTAGACACGTCCAAGAA
     TTGGGGAGGGAGTTCCCAGCTCAGTGGTACAGTCATCTGTGCAGGTTCTT

     ·GlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyr
301  CCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGT
     GGTCAAGAGGGACTTCGACTCGAGACACTGGCGACGCCTGTGCCGGCACA

     ··TyrCysAlaArgGluLysLeuGlyIleGlyAspTyrTrpGlyGlnGly
351  ATTACTGTGCGAGAGAAAAACTGGGGATTGGAGACTACTGGGGCCAGGGA
     TAATGACACGCTCTCTTTTTGACCCCTAACCTCTGATGACCCCGGTCCCT

     ThrLeuValThrValSerSerAlaSerThrLysGlyProSerValPhePro
401  ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
     TGGGACCAGTGGCAGAGGAGTCGGAGGTGGTTCCCGGGTAGCCAGAAGGG

     ·LeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeuGlyCys
451  CCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCCTGGGCT
     GGACCGCGGGACGAGATCTTCGTGGAGGCTCTCGTGTCGGCGGGACCCGA

     ··LeuValLysAspTyrPheProGluProValThrValSerTrpAsnSer
501  GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCA
     CGGACCAGTTCCTGATGAAGGGGCTTGGCCACTGCCACAGCACCTTGAGT

     GlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer
551  GGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTC
     CCGCGAGACTGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGTCAGGAG
```

FIGURE 42 Continuation

```
        GlyLeuTyrSerLeuSerSerValValThrValProSerSerAsnPheGly
601     AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCG
        TCCTGAGATGAGGGAGTCGTCGCACCACTGGCACGGGAGGTCGTTGAAGC

        ThrGlnThrTyrThrCysAsnValAspHisLysProSerAsnThrLys
651     GCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAG
        CGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTCGGGTCGTTGTGGTTC

        ValAspLysThrVal
701     GTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGC
        CACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCCACAGACG

751     TGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCC
        ACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACACGTCGG

801     CCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCC
        GGTCGGGTCCCGTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGCCTCCGG

851     TCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCAC
        AGACGGGCGGGGTGAGTACGAGTCCCTCTCCCAGAAGACCGAAAAAGGTG

901     CAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACA
        GTCCGAGGTCCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGGAAGTGT

951     CACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGG
        GTGTCCCCGTCCACGAACCGAGTCTGGACGGTTTTCGGTATAGGCCCTCC

1001    ACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCT
        TGGGACGGGGACTGGATTCGGCTGGGGTTTCCGGTTTGACAGGTGAGGGA

1051    CAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCT
        GTCGAGCCTGTGGAAGAGAGGAGGGTCTAGGCTCATTGAGGGTTAGAAGA

                GluArgLysCysCysValGluCysProProCysPro
1101    CTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGC
        GAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTCCATTCG

1151    CAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTA
        GTCGGGTCCGGAGCGGGAGGTCGAGTTCCGCCCTGTCCACGGGATCTCAT

1201    GCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCA
        CGGACGTAGGTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGTGGAGGT

                       AlaProProValAlaGlyProSerValPheLeuPhePro
1251    TCTCTTCCTCAGCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCC
        AGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAGAAGGGG

        ProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCys
```

FIGURE 42 Continuation

```
1301  CCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTG
      GGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGCAC

      ·ValValValAspValSerHisGluAspProGluValGlnPheAsnTrpTyr·
1351  CGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGT
      GCACCACCACCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGTTGACCA

      ··ValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlu
1401  ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAG
      TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGTGCCCTCCTC

      GlnPheAsnSerThrPheArgValValSerValLeuThrValValHisGln·
1451  CAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCA
      GTCAAGTTGTCGTGCAAGGCACACCAGTCGCAGGAGTGGCAACACGTGGT

      ·AspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysGlyLeu·
1501  GGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCC
      CCTGACCGACTTGCCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCCGG

      ··ProAlaProIleGluLysThrIleSerLysThrLys
1551  TCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGC
      AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTTGGTTTCCACCCTGGGCG

1601  GGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTCTGCCC
      CCCCATACTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGAGACGGG

                                                GlyGlnProArgGlu
1651  TGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA
      ACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGGGCTCTT

      ProGlnValTyrThrLeuProProSerArgGluGluMetThrLysAsnGln·
1701  CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
      GGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTTCTTGGT

      ·ValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaVal·
1751  GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCG
      CCAGTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGC

      ··GluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrPro
1801  TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCT
      ACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGTGGA

      ProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrVal·
1851  CCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGT
      GGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCA

      ·AspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHis·
```

FIGURE 42 Continuation

```
1901  GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
      CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACG

      ··GluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerPro
1951  ATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG
      TACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGC

      GlyLys
2001  GGTAAA
      CCATTT
```

FIGURE 43

```
                    MetArgLeuProAlaGlnLeuLeuGlyLeuLeuLeu
1                   ATGAGGCTCCCCGCTCAGCTCCTGGGGCTCCTGC
                    TACTCCGAGGGGCGAGTCGAGGACCCCGAGGACG

     ··LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
51   TGCTCTGGTTCCCAGGTGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
     ACGAGACCAAGGGTCCACGGTCCACACTGTAGGTCTACTGGGTCAGAGGT

     SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla
101  TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGC
     AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCCG

     ·SerGlnGlyIleLysAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
151  AAGTCAGGGCATTAAAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGA
     TTCAGTCCCGTAATTTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT

     ··AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
201  AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
     TTCGGGGATTCGCGGACTAGATACGACGTAGGTCAAACGTTTCACCCCAG

     ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
251  CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAAT
     GGTAGTTCCAAGTCGCCGTCACCTAGACCCTGTCTTAAGTGAGAGTGTTA

     ·SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
301  CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
     GTCGTCGGACGTCGGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

     ··SerTyrProCysSerPheGlyGlnGlyThrLysLeuGluIleLysArg
351  ATAGTTATCCGTGCAGTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGA
     TATCAATAGGCACGTCAAAACCGGTCCCCTGGTTCGACCTCTAGTTTGCT

     ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
401  ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
     TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

     ·LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
451  GAAATCTGGAACTGCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
     CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

     ··GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
501  GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAAC
     CTCTCCGGTTTCATGTCACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

     SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
551  TCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
     AGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCGTGGATGTCGGA
```

FIGURE 43 Continuation

```
        SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
601     CAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
        GTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

        AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
651     ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
        TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCG

        PheAsnArgGlyGluCys
701     TTCAACAGGGGAGAGTGT
        AAGTTGTCCCCTCTCACA
```

FIGURE 44

```
                          MetLysHisLeuTrpPhePheLeuLeuLeuValAla
1                         ATGAAACATCTGTGGTTCTTCCTCCTGCTGGTGG
                          TACTTTGTAGACACCAAGAAGGAGGACGACCACC

     ··AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
51   CAGCTCCCAGATGGGTCCTGTCCCAGGTGCAGCTGCAGGAGTCGGGCCCA
     GTCGAGGGTCTACCCAGGACAGGGTCCACGTCGACGTCCTCAGCCCGGGT

     GlyLeuValLysProSerGlnThrLeuSerLeuThrCysThrValSerGly
101  GGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCTGG
     CCTGACCACTTCGGAAGTGTCTGGGACAGGGAGTGGACGTGACAGAGACC

     ·AlaSerIleSerSerGlyAlaTyrTyrTrpSerTrpIleArgGlnHisPro
151  TGCCTCCATCAGCAGTGGTGCTTACTACTGGAGTTGGATCCGCCAGCACC
     ACGGAGGTAGTCGTCACCACGAATGATGACCTCAACCTAGGCGGTCGTGG

     ··GlyLysGlyLeuGluTrpIleGlyTyrIleTyrLysSerGluThrSer
201  CAGGGAAGGGCCTGGAGTGGATTGGGTACATCTATAAGAGTGAGACCTCC
     GTCCCTTCCCGGACCTCACCTAACCCATGTAGATATTCTCACTCTGGAGG

     TyrTyrAsnProSerLeuLysSerArgLeuThrLeuSerValAspThrSer
251  TACTACAACCCGTCCCTCAAGAGTCGACTTACCCTATCAGTAGACACGTC
     ATGATGTTGGGCAGGGAGTTCTCAGCTGAATGGGATAGTCATCTGTGCAG

     ·LysAsnGlnPheSerLeuAsnLeuIleSerValThrAlaAlaAspThrAla
301  TAAGAACCAGTTCTCCCTGAACCTGATCTCTGTGACTGCCGCGGACACGG
     ATTCTTGGTCAAGAGGGACTTGGACTAGAGACACTGACGGCGCCTGTGCC

     ··ValTyrTyrCysAlaArgAspLysLeuGlyIleAlaAspTyrTrpGly
351  CCGTGTATTATTGTGCGAGAGATAAACTGGGGATCGCGGACTACTGGGGC
     GGCACATAATAACACGCTCTCTATTTGACCCCTAGCGCCTGATGACCCCG

     GlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyProSerVal
401  CAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGT
     GTCCCTTGGGACCAGTGGCAGAGGAGTCGGAGGTGGTTCCCGGGTAGCCA

     ·PheProLeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeu
451  CTTCCCCCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCC
     GAAGGGGGACCGCGGGACGAGATCTTCGTGGAGGCTCTCGTGTCGGCGGG

     ··GlyCysLeuValLysAspTyrPheProGluProValThrValSerTrp
501  TGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGG
     ACCCGACGGACCAGTTCCTGATGAAGGGGCTTGGCCACTGCCACAGCACC

     AsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGln
551  AACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACA
     TTGAGTCCGCGAGACTGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGT
```

FIGURE 44 Continuation

```
        ·SerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerAsn
601      GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCA
         CAGGAGTCCTGAGATGAGGGAGTCGTCGCACCACTGGCACGGGAGGTCGT

        ··PheGlyThrGlnThrTyrThrCysAsnValAspHisLysProSerAsn
651      ACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAAC
         TGAAGCCGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTCGGGTCGTTG

         ThrLysValAspLysThrVal
701      ACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGT
         TGGTTCCACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCCA

751      GTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGT
         CAGACGACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACA

801      GCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCG
         CGTCGGGGTCGGGTCCCGTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGC

851      GAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTT
         CTCCGGAGACGGGCGGGGTGAGTACGAGTCCCTCTCCCAGAAGACCGAAA

901      TTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCC
         AAGGTGGTCCGAGGTCCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGG

951      TTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCC
         AAGTGTGTGTCCCCGTCCACGAACCGAGTCTGGACGGTTTTCGGTATAGG

1001     GGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCA
         CCCTCCTGGGACGGGGACTGGATTCGGCTGGGGTTTCCGGTTTGACAGGT

1051     CTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAA
         GAGGGAGTCGAGCCTGTGGAAGAGAGGAGGGTCTAGGCTCATTGAGGGTT

                           GluArgLysCysCysValGluCysProProCysPro
1101     TCTTCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAG
         AGAAGAGAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTC

1151     GTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCT
         CATTCGGTCGGGTCCGGAGCGGGAGGTCGAGTTCCGCCCTGTCCACGGGA

1201     AGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCA
         TCTCATCGGACGTAGGTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGT

                                AlaProProValAlaGlyProSerValPheLeu
1251     CCTCCATCTCTTCCTCAGCACCACCTGTGGCAGGACCGTCAGTCTTCCTC
         GGAGGTAGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAG

         PheProProLysProLysAspThrLeuMetIleSerArgThrProGluVal
```

FIGURE 44 Continuation

```
1301   TTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT
       AAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCA

       ·ThrCysValValValAspValSerHisGluAspProGluValGlnPheAsn
1351   CACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA
       GTGCACGCACCACCACCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGT

       ··TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArg
1401   ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGG
       TGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGTGCC

       GluGluGlnPheAsnSerThrPheArgValValSerValLeuThrValVal
1451   GAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGT
       CTCCTCGTCAAGTTGTCGTGCAAGGCACACCAGTCGCAGGAGTGGCAACA

       ·HisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLys
1501   GCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
       CGTGGTCCTGACCGACTTGCCGTTCCTCATGTTCACGTTCCAGAGGTTGT

       ··GlyLeuProAlaProIleGluLysThrIleSerLysThrLys
1551   AAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGG
       TTCCGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTTGGTTTCCACCC

1601   ACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCT
       TGGGCGCCCCATACTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGA

                                                  GlyGlnPro
1651   CTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC
       GACGGGACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGG

       ArgGluProGlnValTyrThrLeuProProSerArgGluGluMetThrLys
1701   CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAA
       GCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTT

       ·AsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle
1751   GAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACA
       CTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGT

       ··AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr
1801   TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC
       AGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG

       ThrProProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeu
1851   ACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCT
       TGTGGAGGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGA

       ·ThrValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerVal
1901   CACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
```

FIGURE 44 Continuation

```
     GTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC

     ··MetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu
1951 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
     ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGAC

     SerProGlyLys
2001 TCTCCGGGTAAA
     AGAGGCCCATTT
```

FIGURE 45

```
                 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeu
1                ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGC
                 TACTCCCAGGGGCGAGTCGAGGACCCCGAGGACG

    ··LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
51   TGCTCTGGTTCCCAGGCGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
     ACGAGACCAAGGGTCCGCGGTCCACACTGTAGGTCTACTGGGTCAGAGGT

     SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla
101  TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGC
     AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCCG

     ·SerGlnAspIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
151  AAGTCAGGACATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGA
     TTCAGTCCTGTAATCTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT

     ··AlaProLysArgLeuIleTyrAlaAlaSerAsnLeuGlnSerGlyVal
201  AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAATTTGCAAAGTGGGGTC
     TTCGGGGATTCGCGGACTAGATACGACGTAGGTTAAACGTTTCACCCCAG

     ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
251  CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAAT
     GGTAGTTCCAAGTCGCCGTCACCTAGACCCTGTCTTAAGTGAGAGTGTTA

     ·SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
301  CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
     GTCGTCGGACGTCGGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

     ··SerTyrProProThrPheGlyGlyGlyThrLysValGluIleLysArg
351  ATAGCTACCCTCCCACTTTCGGCGGAGGGACCAAGGTGGAAATCAAACGA
     TATCGATGGGAGGGTGAAAGCCGCCTCCCTGGTTCCACCTTTAGTTTGCT

     ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
401  ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
     TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

     ·LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
451  GAAATCTGGAACTGCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
     CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

     ··GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
501  GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAAC
     CTCTCCGGTTTCATGTCACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

     SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
551  TCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
     AGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCGTGGATGTCGGA
```

FIGURE 45 Continuation

```
     ·SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
601   CAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
      GTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

     ··AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
651   ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
      TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCG

      PheAsnArgGlyGluCys
701   TTCAACAGGGGAGAGTGT
      AAGTTGTCCCCTCTCACA
```

FIGURE 46

```
                        MetLysHisLeuTrpPhePheLeuLeuLeuValAla
1                       ATGAAACACCTGTGGTTCTTCCTTCTCCTGGTGG
                        TACTTTGTGGACACCAAGAAGGAAGAGGACCACC

      ··AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
51    CAGCTCCCAGATGGGTCCTGTCCCAGGTGCAGCTGCAGGAGTCGGGCCCA
      GTCGAGGGTCTACCCAGGACAGGGTCCACGTCGACGTCCTCAGCCCGGGT

      GlyLeuValLysProSerGluThrLeuSerLeuThrCysThrValSerGly
101   GGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGG
      CCTGACCACTTCGGAAGCCTCTGGGACAGGGAGTGGACGTGACAGAGACC

      ·ValSerIleSerAsnTyrTyrTrpSerTrpIleArgGlnSerProGlyLys
151   TGTCTCCATCAGTAATTACTACTGGAGCTGGATCCGGCAGTCCCCAGGGA
      ACAGAGGTAGTCATTAATGATGACCTCGACCTAGGCCGTCAGGGGTCCCT

      ··GlyLeuGluTrpIleGlyTyrIleTyrTyrSerGlySerProTyrTyr
201   AGGGACTGGAGTGGATTGGATATATCTATTACAGTGGGAGTCCCTATTAC
      TCCCTGACCTCACCTAACCTATATAGATAATGTCACCCTCAGGGATAATG

      AsnProSerLeuLysSerArgValThrIleSerAlaAspThrSerLysAsn
251   AACCCCTCCCTCAAGAGTCGAGTCACTATATCTGCAGACACGTCCAAGAA
      TTGGGGAGGGAGTTCTCAGCTCAGTGATATAGACGTCTGTGCAGGTTCTT

      ·GlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThrAlaIleTyr
301   CCAATTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCATTT
      GGTTAAGAGGGACTTCGACTCGAGACACTGGCGACGCCTGTGCCGGTAAA

      ··TyrCysAlaArgGluLysLeuGlyIleGlyAspTyrTrpGlyGlnGly
351   ATTACTGTGCGAGAGAAAAACTGGGGATTGGAGACTACTGGGGCCAGGGA
      TAATGACACGCTCTCTTTTTGACCCCTAACCTCTGATGACCCCGGTCCCT

      ThrLeuValThrValSerSerAlaSerThrLysGlyProSerValPhePro
401   ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
      TGGGACCAGTGGCAGAGGAGTCGGAGGTGGTTCCCGGGTAGCCAGAAGGG

      ·LeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeuGlyCys
451   CCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCCTGGGCT
      GGACCGCGGGACGAGATCTTCGTGGAGGCTCTCGTGTCGGCGGGACCCGA

      ··LeuValLysAspTyrPheProGluProValThrValSerTrpAsnSer
501   GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCA
      CGGACCAGTTCCTGATGAAGGGGCTTGGCCACTGCCACAGCACCTTGAGT

      GlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer
551   GGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTC
      CCGCGAGACTGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGTCAGGAG
```

FIGURE 46 Continuation

```
        ·GlyLeuTyrSerLeuSerSerValValThrValProSerSerAsnPheGly
601     AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCG
        TCCTGAGATGAGGGAGTCGTCGCACCACTGGCACGGGAGGTCGTTGAAGC

        ··ThrGlnThrTyrThrCysAsnValAspHisLysProSerAsnThrLys
651     GCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAG
        CGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTCGGGTCGTTGTGGTTC

        ValAspLysThrVal
701     GTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGC
        CACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCCACAGACG

751     TGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCC
        ACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACACGTCGG

801     CCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCC
        GGTCGGGTCCCGTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGCCTCCGG

851     TCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCAC
        AGACGGGCGGGGTGAGTACGAGTCCCTCTCCCAGAAGACCGAAAAAGGTG

901     CAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACA
        GTCCGAGGTCCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGGAAGTGT

951     CACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGG
        GTGTCCCCGTCCACGAACCGAGTCTGGACGGTTTTCGGTATAGGCCCTCC

1001    ACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCT
        TGGGACGGGGACTGGATTCGGCTGGGGTTTCCGGTTTGACAGGTGAGGGA

1051    CAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCT
        GTCGAGCCTGTGGAAGAGAGGAGGGTCTAGGCTCATTGAGGGTTAGAAGA

                  GluArgLysCysCysValGluCysProProCysPro
1101    CTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGC
        GAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTCCATTCG

1151    CAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTA
        GTCGGGTCCGGAGCGGGAGGTCGAGTTCCGCCCTGTCCACGGGATCTCAT

1201    GCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCA
        CGGACGTAGGTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGTGGAGGT

                       AlaProProValAlaGlyProSerValPheLeuPhePro
1251    TCTCTTCCTCAGCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCC
        AGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAGAAGGGG

        ProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCys
1301    CCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTG
```

FIGURE 46 Continuation

GGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGCAC

·ValValValAspValSerHisGluAspProGluValGlnPheAsnTrpTyr
1351 CGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGT
GCACCACCACCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGTTGACCA

··ValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlu
1401 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAG
TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGTGCCCTCCTC

GlnPheAsnSerThrPheArgValValSerValLeuThrValValHisGln
1451 CAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCA
GTCAAGTTGTCGTGCAAGGCACACCAGTCGCAGGAGTGGCAACACGTGGT

·AspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysGlyLeu
1501 GGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCC
CCTGACCGACTTGCCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCCGG

··ProAlaProIleGluLysThrIleSerLysThrLys
1551 TCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGC
AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTTGGTTTCCACCCTGGGCG

1601 GGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTCTGCCC
CCCCATACTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGAGACGGG

GlyGlnProArgGlu
1651 TGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA
ACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGGGCTCTT

ProGlnValTyrThrLeuProProSerArgGluGluMetThrLysAsnGln
1701 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
GGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTTCTTGGT

·ValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaVal
1751 GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCG
CCAGTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGC

··GluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrPro
1801 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCT
ACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGTGGA

ProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrVal
1851 CCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGT
GGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCA

·AspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHis
1901 GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACG

FIGURE 46 Continuation

```
        ··GluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerPro
1951    ATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG
        TACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGC

        GlyLys
2001    GGTAAA
        CCATTT
```

FIGURE 47

```
                    MetArgValProAlaGlnLeuLeuGlyLeuLeuLeu
1                   ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGC
                    TACTCCCAGGGGCGAGTCGAGGACCCCGAGGACG

      ··LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
51    TGCTCTGGTTCCCAGGTGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
      ACGAGACCAAGGGTCCACGGTCCACACTGTAGGTCTACTGGGTCAGAGGT

      SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla
101   TCCTCCCTGTCTGCATCTGTCGGAGACAGAGTCACCATCACTTGCCGGGC
      AGGAGGGACAGACGTAGACAGCCTCTGTCTCAGTGGTAGTGAACGGCCCG

      ·SerGlnGlyIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
151   AAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGA
      TTCAGTCCCGTAATCTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT

      ··AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
201   AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
      TTCGGGGATTCGCGGACTAGATACGACGTAGGTCAAACGTTTCACCCCAG

      ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
251   CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAAT
      GGTAGTTCCAAGTCGCCGTCACCTAGACCCTGTCTTAAGTGAGAGTGTTA

      ·SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
301   CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
      GTCGTCGGACGTCGGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

      ··SerTyrProProThrPheGlyProGlyThrLysValAspIleLysArg
351   ATAGTTACCCTCCCACTTTCGGCCCTGGGACCAAGGTGGATATCAAACGA
      TATCAATGGGAGGGTGAAAGCCGGGACCCTGGTTCCACCTATAGTTTGCT

      ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
401   ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
      TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

      ·LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
451   GAAATCTGGAACTGCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
      CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

      ··GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
501   GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAAC
      CTCTCCGGTTTCATGTCACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

      SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
551   TCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
      AGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCGTGGATGTCGGA
```

FIGURE 47 Continuation

```
     SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
601  CAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
     GTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

     AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
651  ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
     TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCG

     PheAsnArgGlyGluCys
701  TTCAACAGGGGAGAGTGT
     AAGTTGTCCCCTCTCACA
```

FIGURE 48

```
                         MetLysHisLeuTrpPhePheLeuLeuLeuValAla
1                        ATGAAACATCTGTGGTTCTTCCTTCTCCTGGTGG
                         TACTTTGTAGACACCAAGAAGGAAGAGGACCACC

      ··AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
51    CAGCTCCCAGATGGGTCCTGTCCCAGGTGCAGCTGCAGGAGTCGGGCCCA
      GTCGAGGGTCTACCCAGGACAGGGTCCACGTCGACGTCCTCAGCCCGGGT

      GlyLeuValLysProSerGluThrLeuSerLeuThrCysThrValSerGly·
101   GGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGG
      CCTGACCACTTCGGAAGCCTCTGGGACAGGGAGTGGACGTGACAGAGACC

      ·GlySerIleSerArgTyrTyrTrpSerTrpIleArgGlnProProGlyLys
151   TGGCTCCATCAGTCGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGA
      ACCGAGGTAGTCAGCAATGATGACCTCGACCTAGGCCGTCGGGGGTCCCT

      ··GlyLeuGluTrpIleGlyTyrValSerTyrSerGlySerThrTyrTyr
201   AGGGACTGGAGTGGATTGGGTATGTCTCTTACAGTGGGAGCACCTACTAC
      TCCCTGACCTCACCTAACCCATACAGAGAATGTCACCCTCGTGGATGATG

      AsnProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsn
251   AACCCCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAA
      TTGGGGAGGGAGTTCTCAGCTCAGTGGTATAGTCATCTGTGCAGGTTCTT

      ·GlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyr
301   CCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGT
      GGTCAAGAGGGACTTCGACTCGAGACACTGGCGACGCCTGTGCCGGCACA

      ··TyrCysAlaArgAspLysLeuGlyIleGlyAspTyrTrpGlyGlnGly
351   ATTACTGTGCGAGAGATAAACTGGGGATTGGAGACTACTGGGGCCAGGGA
      TAATGACACGCTCTCTATTTGACCCCTAACCTCTGATGACCCCGGTCCCT

      ThrLeuValThrValSerSerAlaSerThrLysGlyProSerValPhePro
401   ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
      TGGGACCAGTGGCAGAGGAGTCGGAGGTGGTTCCCGGGTAGCCAGAAGGG

      ·LeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeuGlyCys
451   CCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCCTGGGCT
      GGACCGCGGGACGAGATCTTCGTGGAGGCTCTCGTGTCGGCGGGACCCGA

      ··LeuValLysAspTyrPheProGluProValThrValSerTrpAsnSer
501   GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCA
      CGGACCAGTTCCTGATGAAGGGGCTTGGCCACTGCCACAGCACCTTGAGT

      GlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer
551   GGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTC
      CCGCGAGACTGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGTCAGGAG
```

FIGURE 48 Continuation

```
     ·GlyLeuTyrSerLeuSerSerValValThrValProSerSerAsnPheGly
601   AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCG
      TCCTGAGATGAGGGAGTCGTCGCACCACTGGCACGGGAGGTCGTTGAAGC

     ··ThrGlnThrTyrThrCysAsnValAspHisLysProSerAsnThrLys
651   GCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAG
      CGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTCGGGTCGTTGTGGTTC

      ValAspLysThrVal
701   GTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGC
      CACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCCACAGACG

751   TGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCC
      ACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACACGTCGG

801   CCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCC
      GGTCGGGTCCCGTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGCCTCCGG

851   TCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCAC
      AGACGGGCGGGGTGAGTACGAGTCCCTCTCCCAGAAGACCGAAAAAGGTG

901   CAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACA
      GTCCGAGGTCCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGGAAGTGT

951   CACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGG
      GTGTCCCCGTCCACGAACCGAGTCTGGACGGTTTTCGGTATAGGCCCTCC

1001  ACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCT
      TGGGACGGGGACTGGATTCGGCTGGGGTTTCCGGTTTGACAGGTGAGGGA

1051  CAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCT
      GTCGAGCCTGTGGAAGAGAGGAGGGTCTAGGCTCATTGAGGGTTAGAAGA

              GluArgLysCysCysValGluCysProProCysPro
1101  CTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGC
      GAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTCCATTCG

1151  CAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTA
      GTCGGGTCCGGAGCGGGAGGTCGAGTTCCGCCCTGTCCACGGGATCTCAT

1201  GCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCA
      CGGACGTAGGTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGTGGAGGT

                     AlaProProValAlaGlyProSerValPheLeuPhePro
1251  TCTCTTCCTCAGCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCC
      AGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAGAAGGGG

      ProLysProLysAspThrLeuMetIleSerArgThrProGluValThrCys
```

FIGURE 48 Continuation

```
1301  CCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTG
      GGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGCAC

      ·ValValValAspValSerHisGluAspProGluValGlnPheAsnTrpTyr
1351  CGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGT
      GCACCACCACCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGTTGACCA

      ··ValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlu
1401  ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAG
      TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGTGCCCTCCTC

      GlnPheAsnSerThrPheArgValValSerValLeuThrValValHisGln
1451  CAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCA
      GTCAAGTTGTCGTGCAAGGCACACCAGTCGCAGGAGTGGCAACACGTGGT

      ·AspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysGlyLeu
1501  GGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCC
      CCTGACCGACTTGCCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCCGG

      ··ProAlaProIleGluLysThrIleSerLysThrLys
1551  TCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGC
      AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTTGGTTTCCACCCTGGGCG

1601  GGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTCTGCCC
      CCCCATACTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGAGACGGG

                                           GlyGlnProArgGlu
1651  TGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA
      ACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGGGCTCTT

      ProGlnValTyrThrLeuProProSerArgGluGluMetThrLysAsnGln
1701  CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
      GGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTTCTTGGT

      ·ValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIleAlaVal
1751  GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCG
      CCAGTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGC

      ··GluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrPro
1801  TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCT
      ACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGTGGA

      ProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrVal
1851  CCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGT
      GGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCA

      ·AspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMetHis·
1901  GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
```

FIGURE 48 Continuation

```
      CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACG

      ··GluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerPro
1951  ATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG
      TACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGC

      GlyLys
2001  GGTAAA
      CCATTT
```

FIGURE 49

```
                    MetArgLeuProAlaGlnLeuLeuGlyLeuLeuLeu
1                   ATGAGGCTCCCTGCTCAGCTCCTGGGGCTCCTGC
                    TACTCCGAGGGACGAGTCGAGGACCCCGAGGACG

      ··LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
51    TGCTCTGGTTCCCAGGTGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
      ACGAGACCAAGGGTCCACGGTCCACACTGTAGGTCTACTGGGTCAGAGGT

      SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAla
101   TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGC
      AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCCG

      ·SerGlnGlyIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
151   AAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCGGGGA
      TTCAGTCCCGTAATCTTTACTAAATCCGACCATAGTCGTCTTTGGCCCCT

      ··AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
201   AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
      TTCGGGGATTCGCGGACTAGATACGACGTAGGTCAAACGTTTCACCCCAG

      ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
251   CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAAT
      GGTAGTTCCAAGTCGCCGTCACCTAGACCCTGTCTTAAGTGAGAGTGTTA

      ·SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
301   CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
      GTCGTCGGACGTCGGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

      ··SerTyrProCysSerPheGlyGlnGlyThrLysLeuGluIleLysArg
351   ATAGTTACCCGTGCAGTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGA
      TATCAATGGGCACGTCAAAACCGGTCCCCTGGTTCGACCTCTAGTTTGCT

      ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
401   ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
      TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

      ·LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
451   GAAATCTGGAACTGCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
      CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

      ··GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
501   GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAAC
      CTCTCCGGTTTCATGTCACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

      SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
551   TCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
      AGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCGTGGATGTCGGA
```

FIGURE 49 Continuation

```
        SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
601     CAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
        GTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

        AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
651     ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
        TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCG

        PheAsnArgGlyGluCys
701     TTCAACAGGGGAGAGTGT
        AAGTTGTCCCCTCTCACA
```

FIGURE 50

```
                    MetLysHisLeuTrpPhePheLeuLeuLeuValAla
1                   ATGAAGCATCTGTGGTTCTTCCTCCTGCTGGTGG
                    TACTTCGTAGACACCAAGAAGGAGGACGACCACC

      ··AlaProArgTrpValLeuSerGlnValGlnLeuGlnGluSerGlyPro
51    CAGCTCCCAGATGGGTCCTGTCCCAGGTGCAGCTGCAGGAGTCGGGCCCA
      GTCGAGGGTCTACCCAGGACAGGGTCCACGTCGACGTCCTCAGCCCGGGT

      GlyLeuValLysProLeuGlnThrLeuSerLeuThrCysThrValSerGly
101   GGACTGGTGAAGCCTTTACAGACCCTGTCCCTCACCTGCACTGTCTCTGG
      CCTGACCACTTCGGAAATGTCTGGGACAGGGAGTGGACGTGACAGAGACC

      ·GlySerIleSerSerGlyValTyrTyrTrpSerTrpIleArgGlnHisPro
151   TGGCTCCATCAGCAGTGGTGTTTACTACTGGAGCTGGATCCGCCAGCACC
      ACCGAGGTAGTCGTCACCACAAATGATGACCTCGACCTAGGCGGTCGTGG

      ··GlyLysGlyLeuGluTrpIleGlyTyrIleTyrAsnSerLysThrSer
201   CAGGGAAGGGCCTGGAGTGGATTGGGTACATCTATAACAGTAAGACCTCC
      GTCCCTTCCCGGACCTCACCTAACCCATGTAGATATTGTCATTCTGGAGG

      TyrTyrAsnProSerLeuLysSerArgLeuThrLeuSerValAspThrSer
251   TATTATAATCCGTCCCTCAAGAGTCGACTTACCCTATCAGTAGACACGTC
      ATAATATTAGGCAGGGAGTTCTCAGCTGAATGGGATAGTCATCTGTGCAG

      ·LysAsnGlnPheSerLeuAsnLeuIleSerValThrAlaAlaAspThrAla
301   TAAGAACCAGTTCTCCCTGAACCTGATCTCTGTGACTGCCGCGGACACGG
      ATTCTTGGTCAAGAGGGACTTGGACTAGAGACACTGACGGCGCCTGTGCC

      ··ValTyrTyrCysAlaArgAspLysLeuGlyIleAlaAspTyrTrpGly
351   CCGTGTATTACTGTGCGAGAGATAAATTGGGGATCGCGGACTACTGGGGC
      GGCACATAATGACACGCTCTCTATTTAACCCCTAGCGCCTGATGACCCCG

      GlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyProSerVal
401   CAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGT
      GTCCCTTGGGACCAGTGGCAGAGGAGTCGGAGGTGGTTCCCGGGTAGCCA

      ·PheProLeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeu
451   CTTCCCCCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCCGCCC
      GAAGGGGGACCGCGGGACGAGATCTTCGTGGAGGCTCTCGTGTCGGCGGG

      ··GlyCysLeuValLysAspTyrPheProGluProValThrValSerTrp
501   TGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGG
      ACCCGACGGACCAGTTCCTGATGAAGGGGCTTGGCCACTGCCACAGCACC

      AsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGln
551   AACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACA
      TTGAGTCCGCGAGACTGGTCGCCGCACGTGTGGAAGGGTCGACAGGATGT
```

FIGURE 50 Continuation

```
        ·SerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerAsn
601     GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCA
        CAGGAGTCCTGAGATGAGGGAGTCGTCGCACCACTGGCACGGGAGGTCGT

        ··PheGlyThrGlnThrTyrThrCysAsnValAspHisLysProSerAsn
651     ACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAAC
        TGAAGCCGTGGGTCTGGATGTGGACGTTGCATCTAGTGTTCGGGTCGTTG

        ThrLysValAspLysThrVal
701     ACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGT
        TGGTTCCACCTGTTCTGTCAACCACTCTCCGGTCGAGTCCCTCCCTCCCA

751     GTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGT
        CAGACGACCTTCGGTCCGAGTCGGGAGGACGGACCTGCGTGGGGCCGACA

801     GCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCG
        CGTCGGGGTCGGGTCCCGTCGTTCCGTCCGGGGTAGACAGAGGAGTGGGC

851     GAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTT
        CTCCGGAGACGGGCGGGGTGAGTACGAGTCCCTCTCCCAGAAGACCGAAA

901     TTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCC
        AAGGTGGTCCGAGGTCCGTCCGTGTCCGACCCACGGGGATGGGGTCCGGG

951     TTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCC
        AAGTGTGTGTCCCCGTCCACGAACCGAGTCTGGACGGTTTTCGGTATAGG

1001    GGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCA
        CCCTCCTGGGACGGGGACTGGATTCGGCTGGGGTTTCCGGTTTGACAGGT

1051    CTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAA
        GAGGGAGTCGAGCCTGTGGAAGAGAGGAGGGTCTAGGCTCATTGAGGGTT

                       GluArgLysCysCysValGluCysProProCysPro
1101    TCTTCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAG
        AGAAGAGAGACGTCTCGCGTTTACAACACAGCTCACGGGTGGCACGGGTC

1151    GTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCT
        CATTCGGTCGGGTCCGGAGCGGGAGGTCGAGTTCCGCCCTGTCCACGGGA

1201    AGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCA
        TCTCATCGGACGTAGGTCCCTGTCCGGGGTCGACCCACGACTGTGCAGGT

                           AlaProProValAlaGlyProSerValPheLeu
1251    CCTCCATCTCTTCCTCAGCACCACCTGTGGCAGGACCGTCAGTCTTCCTC
        GGAGGTAGAGAAGGAGTCGTGGTGGACACCGTCCTGGCAGTCAGAAGGAG

        PheProProLysProLysAspThrLeuMetIleSerArgThrProGluVal
```

FIGURE 50 Continuation

```
1301   TTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT
       AAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCA

       ·ThrCysValValValAspValSerHisGluAspProGluValGlnPheAsn
1351   CACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA
       GTGCACGCACCACCACCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGT

       ··TrpTyrValAspGlyValGluValHisAsnAlaLysThrLysProArg
1401   ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGG
       TGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGTGCC

       GluGluGlnPheAsnSerThrPheArgValValSerValLeuThrValVal
1451   GAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGT
       CTCCTCGTCAAGTTGTCGTGCAAGGCACACCAGTCGCAGGAGTGGCAACA

       ·HisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLys
1501   GCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
       CGTGGTCCTGACCGACTTGCCGTTCCTCATGTTCACGTTCCAGAGGTTGT

       ··GlyLeuProAlaProIleGluLysThrIleSerLysThrLys
1551   AAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGG
       TTCCGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTTGGTTTCCACCC

1601   ACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCT
       TGGGCGCCCCATACTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGA

                                                GlyGlnPro
1651   CTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC
       GACGGGACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGG

       ArgGluProGlnValTyrThrLeuProProSerArgGluGluMetThrLys
1701   CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAA
       GCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTT

       ·AsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle
1751   GAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACA
       CTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGT

       ··AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThr
1801   TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC
       AGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG

       ThrProProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeu
1851   ACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCT
       TGTGGAGGGTACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGA

       ·ThrValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerVal
1901   CACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
```

FIGURE 50 Continuation

```
      GTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC

      ··MetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeu
1951  TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
      ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGAC

      SerProGlyLys
2001  TCTCCGGGTAAA
      AGAGGCCCATTT
```

FIGURE 51

```
                MetArgValProAlaGlnLeuLeuGlyLeuLeuLeu
1               ATGAGGGTCCCTGCTCAGCTCCTGGGGCTCCTGC
                TACTCCCAGGGACGAGTCGAGGACCCCGAGGACG

      ··LeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGlnSerPro
51    TGCTCTGGTTCCCAGGTGCCAGGTGTGACATCCAGATGACCCAGTCTCCA
      ACGAGACCAAGGGTCCACGGTCCACACTGTAGGTCTACTGGGTCAGAGGT

      SerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgThr
101   TCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGAC
      AGGAGGGACAGACGTAGACATCCTCTGTCTCAGTGGTAGTGAACGGCCTG

      ·SerGlnGlyIleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLys
151   AAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGA
      TTCAGTCCCGTAATCTTTACTAAATCCGACCATAGTCGTCTTTGGTCCCT

      ··AlaProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
201   AAGCCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
      TTCGGGGATTCGCGGACTAGATACGACGTAGGTCAAACGTTTCACCCCAG

      ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIle
251   CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAAT
      GGTAGTTCCAAGTCGCCGTCACCTAGACCCTGTCTTAAGTGAGAGTGTTA

      ·SerSerLeuGlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsn
301   CAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATA
      GTCGTCGGACGTCGGACTTCTAAAACGTTGAATAATGACAGATGTCGTAT

      ··SerTyrProProThrPheGlyGlyGlyThrLysValGluIleLysArg
351   ATAGCTACCCTCCCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGA
      TATCGATGGGAGGGTGAAAGCCGCCTCCCTGGTTCCACCTCTAGTTTGCT

      ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeu
401   ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
      TGACACCGACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAA

      ·LysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArg
451   GAAATCTGGAACTGCTAGCGTTGTGTGCCTGCTGAATAACTTCTATCCCA
      CTTTAGACCTTGACGATCGCAACACACGGACGACTTATTGAAGATAGGGT

      ··GluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsn
501   GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAAC
      CTCTCCGGTTTCATGTCACCTTCCACCTATTGCGGGAGGTTAGCCCATTG

      SerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu
551   TCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
      AGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCGTGGATGTCGGA
```

FIGURE 51 Continuation

```
        ·SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyr
601     CAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
        GTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAGA

        ··AlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer
651     ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
        TGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCTCG

        PheAsnArgGlyGluCys
701     TTCAACAGGGGAGAGTGT
        AAGTTGTCCCCTCTCACA
```